STIC-Biotech/ChemLib

145922

From	:
Sant.	

Swope, Sheridan

Tuesday, February 22, 2005 4:59 PM STIC-Biotech/ChemLib

To: Subject:

10/018,964

For 10/018,964, pls search and interference search:

SID 3, residues 1-15, against the NT and AA data bases.

Please separate out the interference searches.

Sheridan Swope, Ph.D.
Patent Examiner, AU 1652
Recombinant Enzymes
571-272-0943 (voice)
E02B71 Remsen Bld (Office)
E02C70 Remsen Bld (Mailbox)

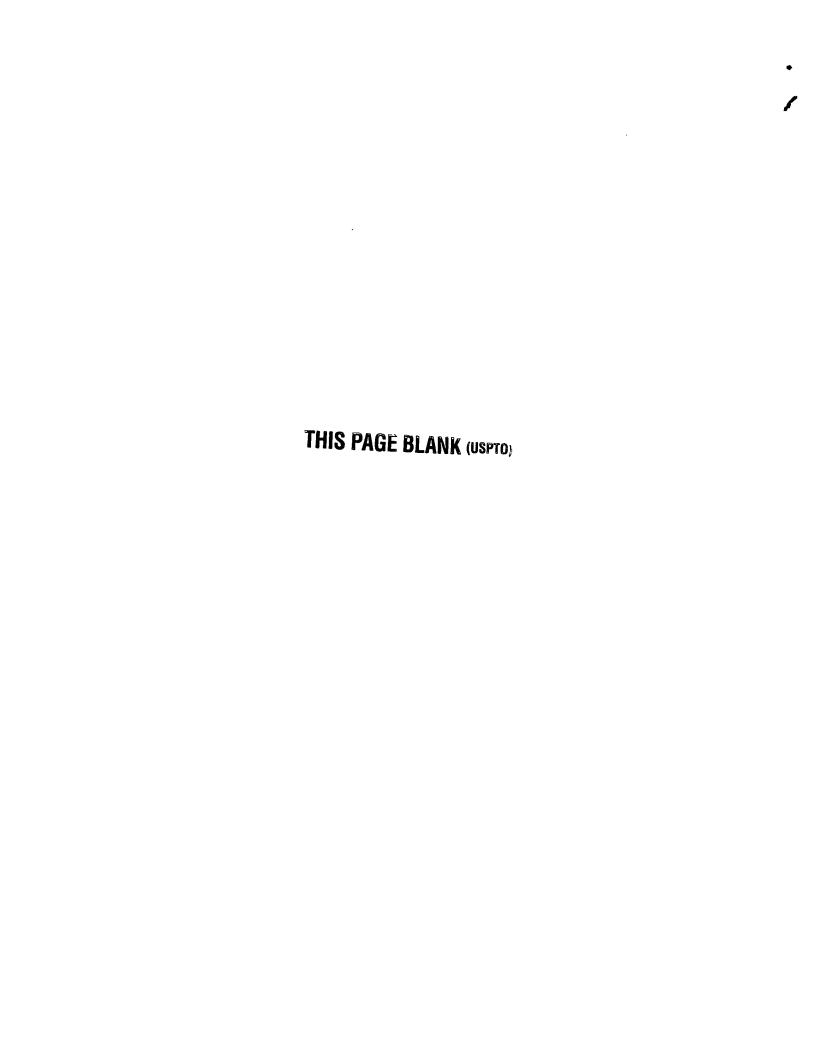
Boypo, Bulow

STAFF USE ONLY

Searcher: ______ Searcher Phone: 2Date Searcher Picked up: _____ Date Completed: _____ Searcher Prep/Rev. Time: _____ Online Time: _____

Type of Search	
NA Sequence: #	
AA Sequence :#	
Structure: #	
Bibliographic:	
Litigation:	
Patent Family:	
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endors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other(Specify):



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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                Copyright
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OM protein - protein search, using sw model

March 3, 2005, 13:50:51; Search time 170 Seconds Run on:

(without alignments) 45.183 Million cell updates/sec US-10-018-964-3 COPY_1_15

1 YSGPPSGARRNCYE 15 score: Sequence: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries DB seq length: 0 DB seq length: 200000000 Maximum

UniProt_03:*

1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P15172 homo gapien		bos t	Q7ys82 bos taurus	P49811 sus scrofa	P29331 ovis aries	P10085 mus musculu	Q02346 rattus norv	Q8c6b1 mus musculu	P21572 coturnix co		-	P13904 xenopus lae		physcom	Q75v42 physcomitre	Q7t109 xenopus tro	Q8wsw9 dugesia tig	Q8wsx0 dugesia tig	P15407 homo sapien	P48755 mus musculu	Q7tmu4 mus musculu	P10158 rattus norv			Q9u966 eimeria ten	Q7xe93 oryza sativ		Ofzar3 oryza sativ		P63977 mycobacteri
SUMMARIES	ID	MYOD HUMAN	075321	077799	Q7YS82	MYOD PIG	MYOD SHEEP	MYOD MOUSE	MYOD_RAT	Q8C6B1	MYOD COLJA	Q6DV59	MYOD_CHICK	MYOD XENLA	Q8AVZ0	Q75V41	Q75V42	Q7T109	O8WSW9	Q8WSX0	FRA1 HUMAN	FRA1 MOUSE	Q7TMU4	FRA1_RAT	Q8WSX1	Q7RRD0	996060	Q7XE93	Q9ZWYS	Q6ZAR3	DP3A MYCBO	DP3A MYCTU
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d	Query Match	100.0	100.0	9.96	9.96	9.96	96.6	72.4	72.4	72.4	69.0	69.0	69.0	65.5	65.5	57.5	57.5	56.9	55.2	55.2	54.0	54.0	54.0	54.0	54.0	54.0	52.9	52.3	51.7	51.7	51.7	51.7
	Score	87	87	84	84	84	84	63	63		9	9	9	57	57	20	20	49.5	48	48	47	47	47	47	47	47	46	45.5	45	45	45	45
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Q05400 streptomyce Q7q307 anopheles g Q7zug9 brachydanio P16076 xenopus lae Q6gn48 xenopus lae Q84w52 arabidopsis Q91fb9 arabidopsis Q9a9j5 caulobacter Q8pay6 xanthomonas Q61hg2 photobacter Q8mm82 caenorhabdi Q8mg148 chlorobium Q8gj49 chlorobium
Q05400 Q7Q307 Q7Q307 MP25_XENLA Q6GN48 Q84W52 Q9LRB9 Q9LRB9 Q9A9J5 Q9LHG2 Q6LHG2 Q6LHG2 Q6GJ49 Q6GJ49
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ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseaisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVIEW ABOUT ACETYLATION AND DEACETYLATION.

MEDLINE=21423399; PubMed=11532390; DOI=10.1016/S0959-437X(00)00224-0; MCKinsey T.A., Zhang C.L., Olson B.N.;

"Control of muscle development by dueling HATe and HDACs.";

Curr. Opin. Genet. Dev. 11:497-504(2001).

-!- FUNCTION: Involved in muscle differentiation (myogenic factor).

Induces fibroblasts to differentiate into myoblasts. Activates muscle-specific promoters. Interacts with and is inhibited by the twist protein. This interaction probably involves the basic domains of both proteins (By similarity).

-!- SUBUNIT: Efficient DNA binding requires dimerization with another bHIH protein. Seems to form active heterodimers with ITF-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUB=Skeletal muscle;
MEDLINE=90059960; PubMed=2583111;
Braun T., Bober E., Buschhausen-Denker G., Kotz S., Grzeschik K.-H.,
Arnold H.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Different:"; cells: possible autoactivation of myogenic determination genes in muscle cells: possible autoactivation by the Myf gene products."; EMBO J. 8:3617-3625(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PTM: Acetylated by a complex containing EP300 and PCAF. The acetylation is essential to activate target genes. Coversly, it decacetylation by SIRT1 inhibits its function (By similarity).
                                                                                                                                                                                                                   Euteleostomi;
                                                                                01-APR-1990 (Rel. 14, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
05-UUD-2004 (Rel. 44, Last annotation update)
Myoblast determination protein 1 (Myogenic factor 3) (Myf-3).
Name=MYOD1; Synonyms=MYF3, MYOD;
Homo sapiens (Human).
                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDI-INE-91212198; PubMed=1850513;
Pearzen-White S.H.;
"Human MyOD: CDNA and deduced amino acid sequence.";
Nucleic Acids Res. 19:1148-1148(1991).
                                          319 AA
                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 53-319 FROM N.A.
                                          STANDARD;
                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                          MYOD HUMAN
RESULT 1
MYOD_HUMAN
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NCBI_TaxID=9913;
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                                                                                                                                               and mouse
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                                                                                                        MIM; 159970; -. Go. 0005634; C:nucleus; TAS.

GO; GO:0005634; C:nucleus; TAS.

GO; GO:0003703; F:RNA polymerase II transcription factor acti. . .; TAS.

GO; GO:0003713; F:transcription coactivator activity; TAS.

GO; GO:0007519; P:myogenesis; TAS.

GO; GO:0006468; P:protein amino acid phosphorylation; TAS.

GO; GO:000637; P:regulation of transcription from Pol II pro. . .; TAS.

InterPro; IPR002546; Basic.

InterPro; IPR01092; HLH_basic.

Pfam; PF01566; Basic.

Pfam; PF01561; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.F., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98206444; PubMed=9546368;
Chen B., Dias P., Jenkins J.J. III, Savell V.H., Parham D.M.;
"Methylation alterations of the MyoDl upstream region are predictive
of subclassification of human rhabdomyosarcomas.";
Am. J. Pathol. 152:1071-1079(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S., Konddinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y., Phelan M., Farmer A.; Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                           Pfam; PF00010; HLH; 1.
PROSITE; PS50888; HLH; 1.
Acetylation; Developmental protein; Differentiation; DNA-binding; Myogenesis; Nuclear protein; Transcription regulation.
Myogenesis; Nuclear protein; Transcription regulation.
DNA_BIND 109 121 Basic motif.
129 121 Helix-loop-helix motif.
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0
                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 87; DB 1; Length 319; 100.0%; Pred. No. 1.6e-05; live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                              124 124 K -> E (in Ref. 2).
319 AA; 34490 MW; AAE935C154318770 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Myogenic determining factor 3 (Myogenic factor 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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            EMBL; X56677; CAA40000.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                     212 YSGPPSGARRENCYE 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 25-OCT-2004 (TrEMBLrel. 28,
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                                                HSSP; P10085; IMDY.
TRANSFAC; T00519; -.
TRANSFAC; T00525; -.
Genew; HGNC:7611; MYODI.
                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100. Matches 15; Conservative
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                                       PIR, S26827; S26827.
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SEQUENCE FROM N.A.
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075321
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DR EMBL; BT00/1...;
DR EMBL; BC064493; AAH644>...
DR EMBL; BC064493; AAH644>...
DR HSSP; PRO08534; C:nucleus; IEA.
DR GO; GO:00005634; C:nucleus; IEA.
DR GO; GO:0000517; F:DNA binding; IEA.
DR GO; GO:000517; P:muscle development; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002546; Basic.
DR InterPro; IPR001092; HLH basic.
DR Fam; PF001091; HLH basic.
DR Pfam; PR001091; HLH; 1.
DR SWART; SW00520; BASIC; 1.
DR SWART; SW00520; BASIC; 1.
DR SWART; SW00520; BASIC; 1.
DR SWART; SW00530; HLH; 1.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50888; HLH; 1.
CW DNA-binding; Nuclear protein.
CROUENCE 320 AA; 34501 WW; 75E624D2ED5B0B33 CRC64;
O: G: Indels 0; G: In
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J., Marra M.A.,
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Am. J. Physiol. Regul. Integr. Comp. Physiol. 280:R1488-R1493(2001).
EMBL, AF093675; AAC63373.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=21193248; PubMed=11294773;
Oldham J.M., Martyn J.A., Sharma M., Jeanplong F., Kambadur R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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Last sequence update)
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Name=MyoD;
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MEDLINE=96024096; PubMed=7559997;
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P29331;
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MYOD SHEEP
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Muroya S., Nakajima I., Chikuni K.;

Muroya S., Nakajima I., Chikuni K.;

Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.

1. SUBMIT: Efficient DNA binding requires dimerization with another bHLH protein (By similarity).

1. SUBMIT: Efficient DNA binding requires dimerization with another bHLH protein (By similarity).

2. SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.

BMBL; ABIIOS99; MAC76802.1; ...

CO: GO:0005634; C:nucleus; IEA.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0005635; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR001092; HLH basic.

R InterPro; IPR001092; HLH basic.

R Ffam; PP010186; Basic; 1.

SWART; SM00520; BASIC; 1.

SWART; SM00520; BASIC; 1.

SWART; SM00539; HLH; 1.

CW DNA-binding; Nuclear protein.

SEQUENCE 318 AA; 34207 MW; BD467B506D0A5447 CRC64;
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                 ;
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                                    96.6%; Score 84; DB 2; Length 150; 93.3%; Pred. No. 2.2e-05; Live 1; Mismatches 0; Indels
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150 AA; 15226 MW; 0C62897AC3D6A477 CRC64;
                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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01-OCT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Name-MYOD1; Synonyms=MYOD;
Sus scrofa (Pig)
                                                                                                                                                                                                                                                                    318 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   319 AA
                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 YSGPPSGARRRNCYD 227
                                                                                                                      1 YSGPPSGARRRNCYE 15
                                                                                                                                           45 YSGPPSGARRRNCYD 59
                                                                                                                                                                                                                                                                                                        01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26,
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                                                                           14; Conservative
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Matches 14; Conservative
                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9913;
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ID MYOD_PIG
AC P49811;
SEQUENCE
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077882

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AC 0778

BE MyOD

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Chang K.C., Fernandes K., Chantler P.D.;

"Cloning and in vivo expression of the pig MyoD gene.";

"Cloning and in vivo expression of the pig MyoD gene.";

J. Muscle Res. Cell Motil. 16:243-247(1995).

-I- FUNCTION: Involved in muscle differentiation (myogenic factor).

Induces fibroblasts to differentiate into myoblasts. Activates
muscle-specific promoters. Interacts with and is inhibited by the
twist protein. This interaction probably involves the basic
domains of both proteins (By similarity).

-I- SUBUNIT: Efficient DNA binding requires dimerization with another
billing protein. Seems to form active heterodimers with ITF-2 (By
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MEDLINB=92158635; PubMed=1741269;

MEDLINB=92158635; PubMed=1741269;

MEDLINB=92158635; PubMed=1741269;

Muclectide sequence of the sheep MyoDl gene.";

Nucleic Acids Res. 20:374-374(1992).

-! FUNGTION: Involved in muscle differentiation (myogenic factor).

-! FUNGTION: Toroblasts to differentiate into myoblasts. Activates muscle-specific promoters. Interacts with and is inhibited by the twist protein. This interaction probably involves the basic
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    similarity).
    SUBCELULAR LOCATION: Nuclear.
    PTM: Acetylated by a complex containing BP300 and PCAF. The acetylation is essential to activate target genes. Coverally, it decacetylation by SIRT1 inhibits its function (By similarity).
    SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.

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Acetylation; Developmental protein; Differentiation; DNA-binding; Myogenesis; Nuclear protein; Transcription regulation.
DNA BIND 1091 121
BABAIN 122 161
Helix-loop-helix motif.
SRQUENCE 319 AA; 34243 MW; B84E5ASCRCF9E288 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovie.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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01-DEC-1992 (Rel. 24, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002546; Basic.
InterPro; IPR001092; HLH basic.
Pfam; PF01586; Basic; 1.
Pfam; PF00010; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U12574; AAA87061.1; -. HSSP; P10085; 1MDY.
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ACETYLATION.
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                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
domains of both proteins (By similarity).
SUBUNIT: Efficient DNA binding requires dimerization with another
bHLH protein. Seems to form active heterodimers with ITF-2 (By
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BEDLINESERS0808185; PubMed=3690668; DOI=10.1016/0092-8674(87)90585-X;
Davis R.L., Weintraub H., Lassar A.B.;
"Expression of a single transfected cDNA converts fibroblasts to
                                                                           SUBSCELLULAR LOCATION: Nuclear.

FUR: Acetylated by a complex containing EP300 and PCAF. The acetylation is essential to activate target genes. Coversly, it decacetylation by SIRT1 inhibits its function (By similarity).

SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
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BEDLINES-2093599; PubMed=1754380; Zingg J.M., Alva G.P., Jost J.P.; (Characterisation of a genomic clone covering the structural mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-89019371; PubMed-3175662;
Tapscott S.J., Davis R.L., Thayer M.J., Cheng P.-F., Weintraub H.,
Lassar A.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PSS6888; HLH; 1.
Acetylation; Developmental protein; Differentiation; DNA-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 84; DB 1; Length 319;
Pred. No. 4.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 161 Helix-loop-helix motif.
319 AA; 34209 MW; 92ECB27BAD568E0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myogenesis; Nuclear protein; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-1989 (Rel. 10, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
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Nucleic Acids Res. 19:6433-6439(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myoblast determination protein 1. Name=Myod1; Synonyms=Myod; Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P10085; IMDY.
InterPro; IPR002546; Basic.
InterPro; IPR001092; HLH_basic.
Pfam; PP01586; Basic; 1.
Pfam; PF01010; HLH; 1.
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P10085;
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MEDLINE=21423399; PubMed=11532390; DOI=10.1016/S0959-437X(00)00224-0; MCKINEST. Zhang C.L., Olson B.N.;

MCKINEST T.A., Zhang C.L., Olson B.N.;

Curr. Opin. Genet. Dev. 11:497-504(2001).

-! FUNCTION: Involved in muscle differentiation (myogenic factor).

-! FUNCTION: Involved in muscle differentiation (myogenic factor).

Induces fibroblasts to differentiate into myoblasts. Activates muscle-specific promoters. Interacts with and is inhibited by the twist protein. This interaction probably involves the basic domains of both proteins.

-!- SUBUNIT: Efficient DNA binding requires dimerization with another belin protein. Seems to form active heterodimers with ITF-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Nuclear.
-!- PTM: Acetylated by a complex containing EP300 and PCAF. The acetylation is essential to activate target genes. Coversly, its decacetylation by STRT1 inhibits its function.
-!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
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Hamamori Y., Wu H.Y., Sartorelli V., Kedes L.;
"The basic domain of myogenic basic helix-loop-helix (bHLH) proteins
is the novel target for direct inhibition by another bHLH protein,
"MyoD1: a nuclear phosphoprotein requiring a Myc homology region to convert fibroblasts to myoblasts."; Science 242:405-411(1988).
                                                                                                                                                                                                                                                                                   Pinney D.F., Pearson-White S.H., Konleczny S.F., Latham K.E., Emerson C.P. Jr., "Myogenic lineage determination and differentiation: evidence for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 102-166.
MEDLINE=94236689; PubMed=8181063; DOI=10.1016/0092-8674(94)90159-7;
Ma P.C.M., Rould M.A., Weintraub H., Pabo C.O.;
"Crystal structure of MyoD bHLH domain-DNA complex: perspectives on DNA recognition and implications for transcriptional activation.";
Cell 77:451-459(1994).
                                                                                                                                                                                                                                           MEDLINE=88223371; PubMed=3286015; DOI=10.1016/0092-8674(88)90095-5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              regulatory gene pathway.";
Cell 53:781-793(1988).
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Mol. Cell 12:51-62(2003).
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PIR; JC1171; JC1171.
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E 116:223-230(1992).

Induces fibroblasts to differentiate into myoblasts. Activates muscle-specific promoters. Interacts with and is inhibited by the twist protein. This interaction probably involves the basic domains of both proteins (By similarity).

SUBUNIT: Efficient DNA binding requires dimerization with another bHLM protein. Seems to form active heterodimers with ITF-2 (By
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: Acetylated by a complex containing EP300 and PCAF. The acetylation is essential to activate target genes. Coversly, its decacetylation by SIRT1 inhibits its function (By similarity). SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
                                                                                                                                                                 3D-structure, Acetylation, Developmental protein, Differentiation, DNA-binding, Myogenesis, Nuclear protein; Transcription regulation. DNA BIND 109 121 Heast motif.

Helix-loop-helix motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92339895; PubMed-1321778; DOI=10.1016/0378-1119(92)90519-U; Vaidya T.B., Rhodes S.J., Moore J.L., Sherman D.A., Konieczny S.F.,
                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                 72.4%; Score 63; DB 1; Length 318; 73.3%; Pred. No. 0.096; 1ve 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Taparowsky E.J.; "Isolation and structural analysis of the rat MyoD gene.";
                                                                                                                                                                                                                                                                                                                  34218 MW; 48C836896FCBDC0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    318 AA
PDB; 1MDY; X-ray; A/B/C/D=-.
TRANSFAC; T00526; -
MGD; MGI: 97275; Myodi.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:0005515; F:protein binding; IPI.
InterPro; IPR00154; Basic.
InterPro; IPR001092; HLH basic.
Pfam; PF00186; Basic; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myoblast determination protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     212 YSGPPSGPRRQNGYD 226
                                                                                                                                                                                                                                                                                                                                                                  73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                    1 YSGPPSGARRRNCYE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M84176; AAA41661.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Myod1; Synonyms=Myod;
                                                                                                                                                PROSITE, PS50888; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 116:223-230(1992)
                                                                                                                                                                                                                                                  134
140
146
163
163
318 AA;
                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
tes 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYOD RAT
Q02346;
                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                   Query Match
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the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 14, 17 days embryo head cDNA, RIKEN full-length enriched library, clone:3200002016 product:myogenic differentiation 1, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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STRAIN=CS7BL/6J; TISSUE=Head;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                           protein; Differentiation; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                           Myogenesis; Nuclear protein; Transcription regulation; DNA BIND 109 121 Basic motif.

DOMĀIN 122 161 Helix-loon-hellt motif
                                                                                                                                                                                                                                                                                                                                        Helix-loop-helix motif.
; FC43E46BB1287F5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.4%; Score 63; DB 1; 73.3%; Pred. No. 0.096; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
HSSP, P10085; 1MDY.
InterPro; IPR002546; Basic.
InterPro; IPR001092; HLH_basic.
                                                                                                                                                                                                                                                                                                                                                                                  34359 MW;
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STRAIN=C57BL/6J; TISSUE=Head;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 YSGPPSGPRRONGYD 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
                                                                                                            Pfam; PF01586; Basic; 1.
Pfam; PF00010; HLH; 1.
PROSITE; PS50888; HLH; 1.
Acetylation; Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 72.4
Best Local Similarity 73.3
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YSGPPSGARRRNCYE
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                                                                                                                                                                                                                                                                                                                                                                                  318 AA;
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Dev. 4:567-581(1990).

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A Adachi J., Alzawa K., Akahira S., Akimura T., Aono H., Arai A.,

A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

A Hanagaki T., Hara A., Hayatau N., Hiramoto K., Hiraoka T., Kato H.,

Rawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

A Sanaki J., Sanaki D., Shibata K., Shibata C., Sakai C., Sakai C., Sakai C., Sanaki Y., Sanaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

A Sogabe Y., Suzuki H., Tagawa A., Takahashi F., Tanaka T.,

Tejima Y., Toya T., Yamamura T., Yamanaka I., Yasunishi A.,

Sohida K., Yoshino M., Muramatsu M., Hayashizaki Y.,

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

-I- SUBUNIT: Efficient DNA binding requires dimerization with another

C -I- SIMILARITY: Contains I basic helix-loop-helix (bHLH) domain.

R EMBL, AKO76157; BAC362241; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:97275; Myodi.

GO; GO:0005513; C:nucleus; IDA.

GO; GO:0005515; F:protein binding; IPI.

GO; GO:0007515; F:protein binding; IPI.

GO; GO:0007519; F:RNA polymerase II transcription factor acti. . .; TAS.

GO; GO:0007519; F:RNA polymerase II transcription factor acti. . .; TAS.

Interpro; IPR002546; Basic.

Interpro; IPR001092; HiH_basic.

Pfam; PF01586; Basic; 1.

Pfam; PF00100; HiH; 1.

SMART; SM00520; BASIC; 1.
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01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
Myoblast determination protein 1 homolog (Myogenic factor 1).
Name-MYOD1; Synonyme-MF1;
Coturnix coturnix Japonica (Japanese quail).
Bukaryota; Metazas, Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Mateumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., Rurgan Integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
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MEDIJNE=90299129; PubMed=2161591;
de la Brousse C.F., Emerson C.P., Jr.;
"Localized expression of a myogenic regulatory gene, qmf1, in the somite dermatome of avian embryos.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                · ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA-binding; Nuclear protein.
SEQUENCE 318 AA; 34233 MW; AEC6572277A78D54 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 73.3 es 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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P21572;
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MYOD COTJA
DD MYOD COTJA
DT 01-MAY-
DT 01-MAY-
DT 01-MAY-
DT 05-UND-
DE MYODIAI
GN NAME-MY
GN CCULTI
OC BUKATY-
OC Archost
OC Archost
OC Archost
OC Archost
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RN (1]
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RA GE 1a
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                  RAPARA RA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
-I. FUNCTION: Involved in muscle differentiation (myogenic factor).

Activates muscle-specific promoters. Interacts with and is inhibited by the twist protein. This interaction probably involves the basic domains of both proteins (By similarity).

SUBUNIT: Efficient DNA binding requires dimerization with another batta protein. Seems to form active heterodimers with ITF-2.

SUBCELLULAR LOCATION: Wuclear.

-I. SUBCELLULAR LOCATION: Wuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
NCBI_TaxID=9103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50888; HiH; 1.
Developmental protein; Differentiation; DNA-binding; Myogenesis;
Duclear protein; Transcription regulation.
DNA BIND 101 113 Basic motif.
DOMĀIN 114 153 Helix-loop-helix motif.
SEQUENCE 297 AA; 32951 MW; 547F3691083CE4B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.0%; Score 60; DB 1; Length 297; 66.7%; Pred. No. 0.27; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-077-2004 (TrEMBLrel. 28, Created)
25-00T-2004 (TrEMBLrel. 28, Last sequence update)
25-00T-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP, P10085, IMDY.
TRANSFAC; T01551; -
INTERPO; IPR002546; Basic.
InterPro; IPR001092; HILH basic.
INTERPO; IPR011009; Kināse_like.
Pfam; PP01586; Basic; 1.
Pfam; PP00010; HLH; 1.
SMART; SM00520; BASIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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InterPro; IRR001092; HLH_basic.
Pfam; PF01586; Basic; 1.
Pfam; PF00010; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L16686; AAA49495.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 YSGPPCSSRRRNSYD 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YSGPPSGARRRNCYE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 66.7
nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A35874; A35874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
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Q6DV59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Length 298;

DB 1;

69.0%; Score 60; DB 1, 66.7%; Pred. No. 0.27;

Mismatches

2;

113 152 Helix-loop-helix motif. 53 53 P -> A (in Ref. 1). 298 AA; 32990 MW; 1C001869E4657B7A CRC64;

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SMART; SM00353; HLH; 1.
PROSITE; PS50888; HLH; 1.
Developmental protein; Differentiation; DNA-binding; Myogenesis;
                                                   Nuclear protein; Transcription regulation.
DNA BIND 100 112 Basic motif.
DOMAIN 113 152 Helix-loop-hei
 SMART; SM00520; BASIC; 1.
                                                                                                                              Query Match 69.0
Best Local Similarity 66.7
Matches 10; Conservative
                                                                                                     SEQUENCE
                                                                                         CONFLICT
                                                                                                                                                                                                                                                             MYOD_XENLA
 STTTWW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-RROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch)
                                                                                                       ö
                                                                                                                                                                                                                             PICO75; Q90916;
01-APR-1990 (Rel. 14, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Myoblast determination protein 1 homolog (MYOD1 homolog).
Name=MYOD1; Synonyms=CMD1, MYOD;
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=89378745; PubMed=2777078;
Lin Z.Y., Decheene C.A., Eldridge J., Paterson B.M.;
"An avian muscle factor related to MyoD1 activates muscle-specific promoters in nonmuscle calls of different germ-layer origin and in BrdU-treated myoblasts.";
                                                                                                       ö
                                                                          69.0%; Score 60; DB 2; Length 297; 66.7%; Pred. No. 0.27; ive 2; Mismatches 3; Indels
                                                   CD7D16B29EFD5243 CRC64;
                                                                                                                                                                                                                       298 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-SPAFAS; TISSUE-Skeletal muscle;
                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002546; Basic.
InterPro; IPR001092; HLH_basic.
             SWART; SM00353; HLH; 1.
PROSITE; PS50888; HLH; 1.
DNA-binding; Nuclear protein.
SEQUENCE 297 AA; 32906 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X16189; CAA34315.1; -. EMBL; L34006; AAA74374.1; -. PIR; A32872; A32872. THSSP; P10085; 1MDY. TRANSFAC; T01128; -.
                                                                                                                                             1 YSGPPSGARRRNCYE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genes Dev. 3:986-996(1989).
SMART; SM00520; BASIC; 1.
                                                                                                    10; Conservative
                                                                                                                                                                                                                       STANDARD;
                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
                                                                                                                                                                                                                       CHICK
                                                                           Query Match
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CHICK
                                                                                                    Matches
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Pfam; PF01586; Basic; 1. Pfam; PF00010; HLH; 1.

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- DEVELOPMENTAL STAGE: Expression is specific to the mesoderm of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The Xenopus MyoD gene: an unlocalised maternal mRNA predates lineage-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- FUNCTION: Myogenesis.
-i- SUBUNIT: Efficient DNA binding requires dimerization with another
   Gaps
                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scales J.B., Olson E.N., Perry M.;
"Two distinct Xenopus genes with homology to MyoDl are expressed
before somite formation in early embryogenesis.";
Mol. Cell. Biol. 10:1516-1524(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! - SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hopwood N.D., Pluck A., Gurdon J.B.; "MyoD expression in the forming somites is an early response to mesoderm induction in Xenopus embryos."; EMBO J. 8:3409-3417(1989).
   ö
                                                                                                                                                                                                       01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Myoblast determination protein 1 homolog (Myogenic factor 1)
3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restricted expression in the early embryo."; Development 108:669-680(1990).
                                                                                                                                                                                                                                                                                                Kenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bhlh protein.
-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (3)
SEQUENCE FROM N.A.
MEDLINE=90353188; PubMed=2167198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=90205830; Pubmed=1690844;
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90059936; PubMed=2555164;
                                                                         189 YSGPPCSSRRRNSYD 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X16106; CAA34232.1; -. EMBL; M31116; AAA49900.1; -.
                                    1 YSGPPSGARRRNCYE 15
                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                 Name=MYOD; Synonyms=MF1;
                                                                                                                                                                                                                                                                                                                                                         Xenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=8355;
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WEDLINE-22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;

MI Klauener R.D., Colline F.S., Garouse L.H., Derge J.G.,

MI Klauener R.D., Colline F.S., Magner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Bromstein M.J., Usdin T.B., Toshiyuki S., Carninor P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guinarathe P.H.,

Richards S., Worlley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lux,, Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human and mouse C.D.A. sequences."
                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                           Gaps
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MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
     TRANSFAC, TUOGOS, 1471.

TRANSFAC, TUOGOS, 1471.

InterPro; IPRO102546; Basic.

FinerPro; IPRO10524; H.H. basic.

Ffam; PF01866; Basic, 1.

Pfam; PF00010; H.H.; 1.

SMART; SM00120; BASIC; 1.

SMART; SM00131; H.H.; 1.

PROSITE; PS50889; H.H.; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Richardson P.; "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                           65.5%; Score 57; DB 1; Length 289; 60.0%; Pred. No. 0.77; 1. Mismatches 3; Indels
                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                 LQ -> A (in Ref. 2).
D0A985DC66136284 CRC64;
                                                                                                                                                                    Helix-loop-helix motif.
                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                       289 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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289 AA; 32306 MW;
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184 YNSPPCGSRRRNSYD 198
                                                                                                                                                                                                                                                                                    1 YSGPPSGARRRNCYE 15
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                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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P10085; 1MDY.
                                                                                                                                                                                                                                         Local Similarity
les 9; Conserv
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGC52596 protein
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                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                           Query Match
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                     Klein S., Strausberg R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-!- SUBUNIT: Efficient DNA binding requires dimerization with another
bHLH protein (89 similarity).
-!- SIMILARITY: Contains I basic helix-loop-helix (bHLH) domain.
EMBL; BC041190; AAH41190.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                               GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0007517; P:muscle development; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Itoh R., Machida M., Takechi K., Takio S., Fujita T., Hasebe M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Physcomitrella patens (Moss).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Bryophyta,
Bryopsida, Funariidae, Funariales, Funariaceae, Physcomitrella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 50, DB 2; Length 172;
Pred. No. 5.9;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Iton R., Machida M., Takechi K., Takio S., Fujita T., Ha
Takano H.;
"Physcomitrella patens gene for minD2 (PpMinD2).";
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AB125339; BAD18010.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE, PS50888; HiH; 1.
DNA-binding; Nuclear protein.
SEQUENCE 289 AA; 32322 MW; 714985C267FBB972 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 AA; 18049 MW; 1B68C6F15D4EB5B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Plastid division site determinant MinD (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: March 3, 2005, 14:00:07 Job time: 171 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                         InterPro; IPR002546; Basic.
InterPro; IPR001092; HLH basic.
Pfam; PF01586; Basic; 1.
SMART; SM00520; BASIC; 1.
SMART; SM00520; BASIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 YNSPPCGSRRRNSYD 198
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Best Local Similarity 60.00,
Best Local Similarity 60.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YSGPPSGARRRNCYE 15
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Matches 8; Conserva
                                                                                                                                                              HSSP; P10085; 1MDY.
TISSUE=Embryo;
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05-JUL-2004 (
05-JUL-2004 (
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Q75V41
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myogenesis protein
transforming prote
transforming prote
probable dnapolyme
hypothetical prote
myogenesis protein
hypothetical prote
dCMP deaminase (EC
tryptophan synthas
hypothetical prote
probable ATP-depen
hypothetical prote
hypothetical prote
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beta/gamma crystal
hox1.3 protein - r
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pectin methylester
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MyoDl protein - sh
myoblast determina
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myogenic factor 1
myogenic factor CM
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                                                March 3, 2005, 13:42:35 ; Search time 39 Seconds (without alignments) 37.006 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                               283416
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                              283416 segs, 96216763 residues
                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                          summaries
                                 - protein search, using sw model
                                                                              US-10-018-964-3_COPY_1_15
87
                                                                                                                              0.5
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S20086
A21636
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A34783
TVRTFF
H70761
S11911
C319371
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S56665
T48714
H84854
T720430
T47424
B87708
B87708
I65197
T28027
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S35336
E87449
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                                                                                                    1 YSGPPSGARRRNCYE 15
                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext
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Maximum Match 100%
Listing first 45 su
                                                                                                                                                                               seq length: 0
seq length: 200000000
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Match Length DB
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2293
2293
2293
2211
11127
227
11127
237
337
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337
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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65.5
54.0
51.7
50.6
50.6
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Perfect score:
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                                                                                                                                                                               Minimum DB Maximum DB
                                 OM protein
                                                                                                                                                                                                                                           Database :
                                                                                                                                              Searched:
                                                  Run on:
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No.
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	2	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	299, 148, 275, 275, 275, 807, 1310, 41310, 144, 198, 219,	0-00000000000000	147.673 00LJX2 00LJX2 847325 847325 847325 86322 G90000 G90000 MXBB62 14466 12679 138740 126708 C97437	,	hypothetical prote trans-activating tense activating tense for the myoD protein - zeb chorismate synthas hypothetical prote probable ligand-ga hypothetical prote gene 62 protein - tensecin-X - bowin probable antigen 1 hypothetical prote hypothetical prote hypothetical protein hypothetical hypothe	
					ALIGNMENTS			
RESULT S26827 myogen N,Alte	T 1 7 nic factor ernate nam	. 3 - hun les: myol	nan O prote:	in;	myogenic deter	determination factor Myf-3	r My£-3	
C, Date	e: 25-Feb- ession: S2	1994 #se 6827; S(equence 16947	Ä	/ision 26-May-1	995 #text_change	ge 09-Jul-2004	
R; Pea Nucle: A; Tit	rson-White ic Acids R le: Human erence num	, S.H. Ges. 19, MyoD: ci ber: S26	1148, NA and 5827, M	de dit	l Juced amino aci :91212198; PMID	d sequence. :1850513		
A; Acci A; Stat A; Mole	ession: 52 tus: preli ecule type	b82/ minary; : mRNA	nuclei	ซี เม	sid sequence no	t shown; trans	translation not shown	
A; Res A; Croi A; Not R; Brai	idues: 1-3 88-referen e: the nuc un, T.; Bo	19 < PEA: ces: UNJ leotide ber, E.	IPROT: P. sequent Buschl	151 2e hau	72; EMBL:X56677 was submitted t sen-Denker, G.;	, NID:934861; o the EMBL Dat: Kotz, S.; Grz	EMBL:X56677; NID:g34861; PIDN:CAA40000.1; PID:g34862 submitted to the EMBL Data Library, November 1990 Denker, G.; Kotz, S.; Grzeschik, K.H.; Arnold, H.H.	ID:93480 r 1990 ld, H.H
A)Tit.	J. 8, 3617 le: Differ erence num	-3625, J ential e ber: S06	1989 express: 5947; M	ion	BO J. 8, 3617-3625, 1989 Title: Differential expression of myogenic determination genes Reference number: S06947; MUID:90059960; PMID:2583111	termination ge :2583111	nes in muscle cells:	8: possib
A; Mol.	ecule type idues: 53- ss-referen	123,'E',	, 125-31; 3L:X176		3RA> NID:934829; PI	DN:CAA35640.1;	PID:934830	
A,Gen A,Crou A,Map C,Sup C,Key	e: GDB:MYO BB-referen position: erfamily:	D1; MYF3 ces: GDE 11p15.4 human my	3:12070' 1-11p15 7ogenin 3; tran	7; . .4	A;Gene: GDB:MYOD1; MYF3 A;Gross-references: GDB:120707; OMIM:159970 A;Map position: 11p15.4-11p15.4 C;Superfemily: human myogenin C;Keywords: DNA binding; transcription regulation	uo		
Que Best Mato	Query Match Best Local Si Matches 15;	h Similarity 15, Conser	100.0%; larity 100.0%; Conservative C	6 .6.	Score 87; D; Pred. No. 3. 0; Mismatches	DB 2; Length 31 3.9e-06; nes 0; Indels	19; 0; Gaps 0;	
රු සි	1 Y 212 Y	YSGPPSGARRNCYE YSGPPSGARRNCYE	RRNCYE	15 226	10			
RESULT S20086 MyoD1 6 C;Speci C;Accee C;Accee R;Huyne Nucleid A;Refet A;Accee	RESULT 2 S20086 MyoD1 protein - sheep C;Species: Ovis orientalis aries, (C;Date: 19-Feb-1994 #sequence_revi;C;Accession: S20086 R;Huynen, L.; Bass, J.; Gardner, R Nucleic Acids Res. 20, 374, 1992 A;Title: Nucleotide sequence of th A;Reference number: S20086; MUID:9A;Accession: S20086	sheep orients 1994 #sc 0086 ass, J.; es. 20, tide sec ber: \$20	pratalis aries, Ovis #sequence_revision U.; Gardner, R.C.; Sequence of the she S20086; MUID:92158	ies regionalist, of of	prais aries, Ovis ammon aries (dom #sequence_revision 10-Nov-1995 #tex J.; Gardner, R.C.; Bellamy, A.R. 20, 374, 1992 sequence of the sheep MyoD1 gene. S20086; MUID:92158635; PMID:1741269	estic t_char	sheep) nge 09-Jul-2004	

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myogenic factor 1 - Japanese quail
Cispecies: Coturnix coturnix japonica (Japanese quail)
Cispecies: Coturnix coturnix japonica (Japanese quail)
Cispecies: 31-Oct-1990 #sequence_revision 31-Oct-1990 #text_change 09-Jul-2004
CiAccesson: A35874
Circulates de la Brousse, F.; Emerson Jr., C.P.
Genes Dev. 4, 567-581, 1990
A,Fittle: Localized expression of a myogenic regulatory gene, qmfl, in the somite dermaton A,Reference number: A35874
A,Reference number: A35874
A,Accession: A35874
A,Accession: A35874
A,Residues: preliminary
A,Molecule type: mRNA
A,Residues: 1-297 <CHA>
A,Cross-references: UNIPROT: P21572; GB:L16686; NID:g294450; PID:g294451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: An avian muscle factor related to MyoDl activates muscle-specific promoters in r
A;Reference number: A32872; MUID:89378745; PMID:27777078
A;Accession: A32872
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A,Roesidues: 1.298 -LIN>
A)Cross-references: UNTPROT:P16075; EMBL:X16189; NID:g62868; PIDN:CAA34315.1; PID:g62869
A)Cross-references: UNTPROT:P16075; EMBL:X16189; NID:g62868; PIDN:CAA34315.1; PID:g62869
R;Dechesne, C.A.; Wei, Q.; Eldridge, J.; Gannoun-Zaki, L.; Millasseau, P.; Bougueleret, I
Mol. Cell. Bilo. 14, 5474-5486, 1994
Mol. Cell. Bilo. 14, 5474-5486, 1994
A;Title: B-box- and MEF-2-independent muscle-specific expression, positive autoregulation
A;Reference number: A53783; MUID:94309668; PMID:8035824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        myogenic factor CMD1, embryonic skeletal muscle - chicken C;Species: Gallus gallus (chicken) C;Species: Gallus gallus (chicken) C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004 C;Accession: A32872, A53782 C;Accession: A32872, A53782 G;Accession: B.M. Genes Dev. 3, 986-996, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: CMD1
A;Introns: 186/3; 213/1
C;Superfamily: human myogenin
C;Keywords: DNA binding; muscle; skeletal muscle; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-52,'p',54-298 <DEC>
A;Cross-references: GB:L34006; NID:g504490; PIDN:AAA74374.1; PID:g506807
A;Note: authors translated the codon GGA for residue 269 as Ser
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 60; DB 2; Length 298;
Pred. No. 0.06;
2; Mismatches 3; Indels
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                                                                                                                                          Query Match
72.4%; Score 63; DB 2; Length 318;
Best Local Similarity 73.3%; Pred. No. 0.021;
Matches 11; Conservative 2; Mismatches 2; Indels
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A;Introns: 209/3; 236/1
C;Superfamily: human myogenin
C;Keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: human myogenin
C;Keywords: DNA binding; transcription regulation
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Best Local Similarity 66.7%;
Matches 10; Conservative
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Best Local Similarity 66.7
Matches 10; Conservative
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A; Residues: 1-318 < DAVA
A; Cross-references: UNIPROT: P10085; GB: M18779; NID: g199994; PIDN: AAA39799.1; PID: g199995
A; Experimental source: embryonic fibroblast C3H10T1/2 cell line
R; Zingg, J.M.; Alva, G.P.; Jost, J.P.
R; Zingg, J.M.; Alva, G.P.; Jost, J.P.
A; Title: Characterisation of a genomic clone covering the structural mouse MyoD1 gene an A; Reference number: S22587; MUID: 92093599; PMID: 1754380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Accession: JC1171
A, Molecule type: DNA
A, Molecule type: DNA
A, Cross-references: UNIPROT: Q02346; GB: M84176; NID: 9205602; PIDN: AAA41661.1; PID: 9205603
C, Comment: This protein initiates the myogenic program.
C, Genetics:
A, Gene: MyoD
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C;Species: Rattus norvegicus (Norway rat)
C;Apaces: Nat-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JG1171
R;Vaidya, T.B.; Rhodes, S.J.; Moore, J.L.; Sherman, D.A.; Konieczny, S.F.; Taparowsky, Gene 116, 223-230, 1992
A;Title: Isolation and structural analysis of the rat MyoD gene.
A;Reference number: JG1171; MUID:92339895; PMID:1321778
   A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: mRNA A;Rolecule type: mRNA A;Rolecule type: mRNA A;Rolecule type: nulysometary, Embl. (2010; NID:g1347; PIDN:CAA44012.1; PID:g1348 A;Croserreferences: UNIPROT:P29331; EMBL. X62102; NID:g1347; PIDN:CAA44012.1; PID:g1348 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991 C;Superfamily: human myogenin C;Keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                myoblast determination protein, 1 - mouse
NyAlternate names: MyoD1 protein
Cippecies: Miss missellus (house mouse)
Cipacies: Jalwar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
Cipacession: A29636; S22587
Ribaria, R.L.; Weintraub, H.; Lassar, A.B.
Cell 51, 987-1000, 1987
A;Title: Expression of a single transfected cDNA converts fibroblasts to myoblasts.
A;Reference number: A29636; MUID:88080485; PMID:3690668
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-318 <21N>
A, Cross-references: EMBL:X61655; NID:953301; PIDN:CAA43836.1; PID:953302
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                                                                                                                                                                                                                                                                                                    Length 319;
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                                                                                                                                                                                                                                                                                                 Query Match
96.6%; Score 84; DB 2; Length 319
Best Local Similarity 93.3%; Pred. No. 1.1e-05;
Matches 14; Conservative 1; Mismatches 0; Indels
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Pred. No. 0.021;
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C;Superfamily: human myogenin
C;Keywords: DNA binding; transcription regulation
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1 Similarity 73.3%;
11; Conservative
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Best Local Similarity
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Matches

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Gaps

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transforming protein fra-1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: A27722; 157559
R;Cohen, D.R.; Curran, T.
Mol. Cell. Biol. 8, 2063-2069, 1988
A;Title: fra-1: a serum-inducible, cellular immediate-early gene that encodes a fos-rela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-275 < COH>
A; Cross-references: UNIPROT:P10158; GB:M19651; NID:g204174; PIDN:AAA41171.1; PID:g204175
A; Experimental source: Flscher F2408 embryo fibroblast cell line 208F
B; Bergers, G.; Graninger, P.; Braselmann, S.; Wrighton, C.; Busslinger, M.
Mol. Cell. Biol. 15, 3748-3758, 1995
A; Title: Transcriptional activation of the fra-1 gene by AP-1 is mediated by regulatory
A; Reference number: 157559; MUID:95311973; PMID:7791782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: H70761
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, S37-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
                                                                                                                                                                                                                                                                                                            C;Superfamily: fos transforming protein; fos/jun DNA-binding domain homology C;Keywords: DNA binding; nucleus F;100-140/Domain: fos/jun DNA-binding domain homology <FJD>
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C;Comment: This protein is a fos-related antigen (fra) that may bind to DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: fos transforming protein; fos/jun DNA-binding domain homology
C;Reywords: DNA binding; leucine zipper; transforming protein
F;1.02-142/Domain: fos/jun DNA-binding domain homology <FJD>
F;135-163/Region: leucine zipper motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable dnapolymerase III - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
                                                                                                                                                   A;Cross-references: GB:D16365; NID:g537351; PIDN:BAA03867.1; PID:g4433154
C;Genetics:
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Pred. No. 6;
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72.7%; Pred. No. 5.9;
:ive 0; Mismatches
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A;Accession: I56863
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5 <RES>
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Best Local Similarity 72...
Best Local 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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A;Residues: 1-43 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: A27722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Introns: 35/3
                                                                                                                                                                                                                                                                    A;Gene: fra-1
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A; Accession: A60099
A; Molecule type: mRNA
A; Residues: 1-289 < HAR>
C; Genetics: A; Genetics: A; Genetics: C; Function: C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transforming protein (fra-1) - human (5) Cispecies: Home sapiens (man) (5) Cispecies: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 09-Jul-2004 (Cispeciesion: S15750; 156863; $08010 (Cispeciesion: S15750; 156863; $08010 (Cispeciesion: S15750; 15990 (Cispeciesion: S1579) (Cispeciesion: S15749; MUID:90191709; PMID:2107490 (Cispeciesion: S15750) (C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Residues: 1-289 <SCA>
A, Cross-references: UNIPROT: P13904; GB: M31116
R; Hopwood, N.D.: Pluck, A.; Gurdon, J.B.
EMBO J. 8, 3409-3417, 1989
A; Title: MyoD expression in the forming somites is an early response to mesoderm inducti
A; Reference number: S06952; MUID: 90059936; PMID: 2555164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P15407; EMBL:X16707; NID:931462; PIDN:CAA34679.1; PID:931463
R;Tsuchiya, H.; Fujii, M.; Niki, T.; Tokuhara, M.; Matsui, M.; Seiki, M.
Virol. 67, 7001-7007, 1993
A;Title: Human T-cell leukemia virus type 1 Tax activates transcription of the human fra
A;Reference number: 156863; MUID:94047311; PMID:8230424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Pathway: myogenesis; skeletal muscle differentiation
Nyote: expressed exclusively in skeletal muscle and first activated during gastrulation
C;Superfamily: human myogenin G;Keywords: alternative splicing; differentiation; DNA binding; skeletal muscle; transcr
                                                                                                                                                                                                                                                                                                                                           myogenesis protein MyoDa - African clawed frog
N;Alternate names: myoblast determination protein; myogenic factor 1
C;Species Xenopus laevis (African clawed frog)
C;Species Xenopus laevis (African clawed frog)
C;Decies 3.3 Jul-1990 #sequence revision 13-Jul-1990 #text_change 09-Jul-2004
C;Accession: A34783; S0652; A60099
R;Scales, J.B.; Olson, E.N.; Perry, M.
Mol. Cell. Biol. 10, 1516-1524, 1990
A;Title: Two distinct Xenopus genes with homology to MyoDl are expressed before somite A;Reference number: A34783; MUID:90205830; PMID:1690844
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A;Residues: 1-289 <HOP>
A;Cross-references: EMBL:X16106; NID:g64906; PIDN:CAA34232.1; PID:g64907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Description: activates expression of skeletal muscle-specific genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                              189 YSGPPCSSRRRNSYD 203
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Best Local Similarity 60.00
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Development 108, 669-680, 1990
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A;Molecule type: mRNA
A;Residues: 1-271 <MAT>
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Ajntrons: 1827.3
Ajntrons: 1827.3
Ajntrons: 1827.3
Ajntrons: 1827.3
Ajntrons: 1827.3
Ajntrons: Intron list may be incomplete
Ajntrons: Intron list may be incomplete
Ajntrons: activates expression of skeletal muscle differentiation
Ajntrons: expressed exclusively in skeletal muscle and first activated during gastrulation
CjSuperfamily: human myogenin
CjKeywords: differentiation; DNA binding; skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CjAccession: T45957
R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Lemc submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23018
A;Accession: T45957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species: Arabidopsis thaliana (mouse-ear cress)
Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 2; Length 287;
Pred. No. 18;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pothetical protein F7J8.150 - Arabidopsis thaliana
      A;Residues: 2-55,'PE',57-182 <HA2>
                                                                                                                                                                                                                                                                                                                                                       50.64;
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183 NSPPCSSRRRNSYD 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 SGPPSGARRRNCYE 15
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.09
Matches 7; Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
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                                    C,Genetics:
A,Gene: mf25; MyoDb
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A; Note: F7J8.150
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MyAlternate names: myogenic factor 25
CjSpecies a Kenopue laevis (African clawed frog)
CjDate: 13-U1-1990 #sequence revision 13-U1-1990 #text_change 09-U1-2004
CjDate: 13-U1-1990 #sequence revision 13-U1-1990 #text_change 09-U1-2004
CjAccession: C34783; B60099; C60099
R;Scales, J.B.; Olson, EN.; Perry, M.
Mol. Cell. Biol. 10, 1516-1524, 1990
A;Title: Two distinct Xenopus genes with homology to MyoDl are expressed before somite f
A;Reference number: A34783; MUID:90205830; PMID:1690844
A;Reference C34783
A;Molecule type: mRNA
A;Residues: 1-287 <SCA>
A;Cross-references: UNIPROT:P16076; GB:M31118; NID:g214591; PIDN:AAA49902.1; PID:g214592
R;Harvey, R.P.
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Affile: The Xenopus MyoD gene: an unlocalised maternal mRNA predates lineage-restricted
A;Reference number: A60099; MUID:90353188; PMID:2167198
A;Accession: B60099
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70761
A;Accession: H70761
A;Accession: Diaminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1184 <COL>
A;Residues: 1-1184 <COL>
A;COLSA:Cress-references: UNIPROT:Q10779; GB:Z74020; GB:AL123456; NID:g3261584; PIDN:CAA98315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species Streptomyces rimosus
C;Species Streptomyces rimosus
C;Species Streptomyces rimosus
C;Species 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C;Accession: S11911
Mol. Gen. Genet. 222, 129-134, 1990
A;Title: Five transfer RNA genes lacking CCA termini are clustered in the chromosome of A;Reference number: S11911; MUID:91042413; PMID:1700267
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A;Residues: 1-55,'PE',57-66,'E',67-98,'E',100-255,'K',257-281,'N',283-287 <HAR>
A;Note: authors translated the codon GAG for residue 101 as Arg
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                                                                                                                                                                                                                                                                                                                                                                                                                    5; Indels
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C;Superfamily: DNA-directed DNA polymerase III alpha chain
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$11911
hypothetical protein - Streptomyces rimosus (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 50.6%; Score 44; DB 2; Best Local Similarity 88.9%; Pred. No. 9.2; Matches 8; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: not compared with conceptual translation A;Molecule type: DNA
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A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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A,Cross-references: UNIPROT:Q05400
A,Experimental source: strain R6-554
                                                                                                                                                                                                                                                                                                                                                    cuery match
Best Local Similarity 57.1%;
Matches 8; Conservative
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111 PPSGARRRS 119
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A;Residues: 1-949 <STO>
A;Cross-references: UNIPROT:Q9A9J5; GB:AE005673; NID:g13422269; PIDN:AAK22969.1; GSPDB:GR
C;Genetics:
A;Gene: CC0985
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                                                                                                                                                                                                                                                                                                                                               hypothetical protein CC0985 [imported] - Caulobacter crescentus
                                                                                                                                                       Length 568;
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A;Status: preliminary
A;Molecule type: DNA
A;Redidues: 1-568 <BEV>
A;Cross-references: UNIPROT:Q9LFB9; EMBL:AL137189
A;Experimental source: cultivar Columbia; BAC clone F7J8
                                                                                                                                                     Score 44; DB 2;
Pred. No. 32;
3; Mismatches
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2 SGPPSGARRRNCYE 15

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RESULT 15
dCMP deaminase (EC 3.5.4.12) - Cenarchaeum symbiosum
C;Species: Cenarchaeum symbiosum
C;Species: Cenarchaeum symbiosum
C;Species: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: 731322
R;Schleper, C.; DeLong, B.F.; Preston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V.
J. Bacteriol. 180, 5003-5009, 1998
A;Title: Genomic analysis reveals chromosomal variation in natural populations of the ur
A;Reference number: 220994; MUID:98422450; PMID:9748430
A;Accession: T31322
A;Accession: T31322
A;Accession: T31322
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-184 <SCH>
A;Residues: 1-184 <SCH>
A;Cross-references: UNIPROT:074069; EMBL:AF083072; NID:g3599393; PID:g3599408; PIDN:AAC6
C;Genetices:
A;Genetices:
A;G
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                                                                                                 7 SGPPSSFRRRAHK 20
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Gaps 7

Search completed: March 3, 2005, 13:57:11 Job time : 40 secs

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Title: Perfect score:

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X62102 Carries mRN
U12574 Sus scrofa
CQ787414 Sequence
AX59884 Sequence
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AX795747 Sequence
AX822255 Sequence
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AX822359 Sequence
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M84918 M.musculus
X61655 M.musculus
M84176 Rattus norv
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AC103001 Rattus no
AC020796 Mus muscu
AC128796 Rattus no
AC132503 Rattus no
L16686 Coturnix co
AY641567 Meleagris
X16189 Chicken CMD
L34006 Chicken (cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 963)

Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,W., Rappael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Chelan,M. and Farmer,A.

Cloning of human full-length CDSs in BD Creator(TM) System Donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished

2 (bases 1 to 963)

Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Dhelan, M. and Farmer, A.

Direct Submission
                                                                                                                                                                                                                  AC04736 Human Chr
AC124056 Humo sapi
AC05151 Homo sapi
AC124301 Homo sapi
AC124301 Homo sapi
AF093675 Bos tauru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRI 13-MAY-2003
                                                                                                                                                                                                                                                                                                                                 BV012581 myod1sts3
AB110599 Bos tauru
  CQ714840 Sequence
AK77207 Sequence
CQ787200 Sequence
AX598705 Sequence
AX757361 Sequence
AX79566 Sequence
AX822116 Sequence
AX825756 Sequence
AX825756 Sequence
AX82718 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF213004 Peromyscu
                                                                                                                                                                                                     Homo sapi
Human Chr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 Bast Meadow Circle, Palo Alto, CA 94303, USA.
This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       963 bp mRNA linear
Homo sapiens myogenic factor 3 mRNA, complete cds.
BT007157
                                                                                                                                                                                                         AF027148
AC124056-02
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AC05151-02
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AC026496
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AF027148
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CQ787414
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BT007157
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
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REFERENCE
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                 Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-O=/CGD2_1/USPTD spool_p/US10018964/runat_03032005_114706_21361/app_query.fasta_1.199
-DB=GGD2_1/USPTD spool_p/US10018964/runat_0302005_114706_21361/app_query.fasta_1.199
-DB=GGD2_1/GPTD-spool_p/US10018964/runat_03032005_114706_21361/app_query.fasta_1.199
-UNITS-bits -START=1 -END=-1 -MATRIX-bitsomm62 -TRANS-human40.cdi -1.15T=45
-DOCALIGN=200 -THR_SCORE=pct -THR MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAPSTZE=570 -MINLEN=0 -MAXIEN=200000000
-USR=US10018964_@CGN 1 1.5600_@runat_03032005_114706_21361 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-NEW TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BT007157 Homo sapi
BT007461 Synthetic
X17650 Human Myf-3
X56677 Human MyoD
                                                                                                                     7, 2005, 03:44:32 ; Search time 1745 Seconds (without alignments) 416.520 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9416466
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                 nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                     4708233 segs, 24227607955 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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BT007461
HSMYF3
HSMYOD
                                                                                                                                                                                                                US-10-018-964-3_COPY_1_15
                                                                                                                                                                                                                                                                      BLOSUM62
Xgapo 10.0 , Xgapo Ygapox 10.0 , Ygapox 10.0 , Ygapoxt Fqapop 6.0 , Fgapoxt 6.0 , Delext 7.72760
                                                                                                                                                                                                                                                           YSGPPSGARRRNCYE 15
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Database

Score

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This CDS clone is a part of a collection of human full length
This CDS clone generated by BD Biosciences Clontech and the
Harvard Institute of Proteomics. Each CDS has been cloned in two
forms: with and without stop-codon (to allow fusion with C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLI CONA.

synchetic construct
synthetic construct
other sequences;

1 (bases 1 to 963)
Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S.,
Kondinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y.,
Phelan, M. and Farmer, A.
Cloning of human full-length CDSs in BD Creator (TW) System Donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BT007461 963 bp mRNA linear SYN 13-MAY-2003
Synthetic construct Homo sapiens myogenic factor 3 mRNA, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished

2 (bases 1 to 963)

2 (bases 1 to 963)

Koundinya, M., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Phelan,M. and Parmer,A.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="myogenic factor 3"
/protein id="AAP35821.1"
/db xref="GT:30583153"
/tdb xref="GT:30583153"
/translation="MELLSPPLRDVDLTAPDGSLCSFATTDDFYDDFCFDSPDLRFFE
DLDPRLMHVGALLFFEBRISHFPRAVHPPRGAREDEHVRAPSGHHQAGRCLLWACKACK
RKTTNADRRKAATWRERRRLSKVNBAFETLKRCTSSNPNQRLFKVEILRNAIRYIEGL
forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion (TM) cloning system between the Sall and Hindill sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after Sall site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before Hindill site to maintain reading frame. Clone distribution: http://bioinfo.clontech.com/orfclones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QALLRDQDAAPPGAAAAFYAEGPLPPGRGGEHYSGDSDASSPRENCSDGMNDYSGPPS
GARRRNCYEGAYYNEAPSEPRPGKSAAVSSLDCLSSIVERISTESPAAPALLLADVPS
ESPPRRQEAAAPSEGESSGDPTGSPDAAPQCPAGANFNPIYQVL"
                                                                                                                                                                                                                                                                                                                                      /clone_lib="BD Creator(TM) CDS Library derived from MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TyrserGlyProProSerGlyAlaArgArgArgAsnCysTyrGlu 15
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                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DH5alpha T1 resistant"
/note="Vector: pDNR-Dual"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-018-964-3_COPY_1_15 (1-15) x BT007157 (1-963)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
                                                                                                                                                                                                              1. .963
/organism="Homo sapiens"
/mol_type="mRNN"
/db_xref="taxon:9666"
/clone="GH00761X1.0"
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AUTHORS
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tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the SalI and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after Llast codon and before HindIII site to maintain reading frame. Clone distribution: http://bioinfo.clontech.com/orfclones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1416)

Braun, T., Bober, E., Buschhausen-Denker, G., Kohtz, S., Grzeschik, K.H., Arnold, H.H. and Kotz, S.

Grzeschik, K.H., Arnold, H.H. and Kotz, S.

Grzeschik, E.H., Arnold, H.H. and Kotz, S.

Englo, S. (1989)
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Gevelopmental regulation; Myf gene; Myf-3 gene; MyoDl protein;
transcriptional activator.
Homo sapiens
Homo sapiens
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Data kindly reviewed (21-FEB-1990) by Harold H.H.
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Conservative:
Mismatches:
Indels:
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note="Mutations: 962:Stop->Leu"
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Homo sapiens
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Pearson-White, S.H.
Direct Submission
Submitted (19-NOV-1990) S.H. Pearson-White, UNIVERSITY OF VIRGINIA
MEDICAL CENTRE, HSC MR-4 BLDG BOX 1131 ROOM 1127, CHARLOTTESVILLE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1692)
Pearson-White, S.H...
Human Myob: cDNA and deduced amino acid sequence
Nucleic Acids Res. 19 (5), 1148 (1991)
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Matches:
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                                                                                                                                                                                                                                                                                                                                  Mismatches:
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Homo sapiens (human)
Homo sapiens
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121. .1080
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X56677
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Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.R., Bhat, N. K.,
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Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
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QALLRDQDAAPPGAAPFGAPFPGRGGHYSGDSDASSPRSNCSDGMMDYGGPPSG
ARRRNVTGAAYTWEBSEPRPGKSAAVSSLDYLSSIVBRISTESPAPALLLADVPSE
SPPRRQGFAXYBEADSPR
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HOMO Bapiens myogenic factor 3, mRNA (CDNA CLONE MGC:71135
IMAGE:5022419), complete cds.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1699)
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Submitted (12-DE-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Contact: MGC help desk
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Mismatches:
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Tissue Procurement: ATCC
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Strausberg, R.
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Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baranova, A.V., Yankovsky, N.K., Kozlov, A.P., Lobashev, A.V. and Krukovskaya, L.L.
In silico screening for phenotype-associated expressed sequences Patent: WO 02103028-A 400 27-DEC-2002;
Biomedical Center (RU)
    Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TyrSerGlyProProSerGlyAlaArgArgArgAsnCysTyrGlu 15
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Patent: WO 02068579-A 774 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
1. 1757
/organism="Homo sapiens"
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AX677207
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Sequence 50 from Patent W02004020662.
CQ787200
CQ787200.1 GI:45722183
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            Gaithersburg, Maryland;
Web site: http://www.nisc.nh.gov/
Contact: nisc_mgc@nhgrl.nih.gov/
Contact: nisc_mgc@nhgrl.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Grantle,S., Gunn,X., Gupta,J., Haghlghl,P.,
Dietrich,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Peargoon,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 50 Row: f Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23111008. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="MIM:159970"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKTTNADRRKAATWRERRRLSKVNEAPETLKRCTSSNPNQRLPKYETLRNATRYTEGL
OALLBRODDAAAPEGAAAAFYSPGPLPSGRGGEHYSGDSDASSPRSNCSDGMMDYSGPPS
GARRRNCYEGAYYNBAPSEPRPGKSAAVSLDCLSSYVERLSTESPAAPALLLADVPS
ESPPRRQEAAAPSEGESSGDPTQSPDAAPQCPAGANPNPIYQVL
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Seguence 774 from Patent WO02068579.
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CQ714840.1 GI:42275697
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Sequencing Center
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PAT 02-JUL-2003
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whethod and nucleic acids for the analysis of a lung cell
proliferative disorder
Patent: WO 0305135-A 8 26-JUN-2003;
Epigenomics AG (DE)
                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Method and nucleic acids for the analysis of a lymphoid cell
proliferative disorder
Patent: WO 03044226-A 9 30-MAY-2003;
Epigenomics AG (DE)
                                                                                                                                                                                        Burger, M., Caldwell, C., Genc, B., Becker, E., Maier, S. and
Nimmrich, I.
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Sequence 8 from Patent WO03052135.
AX795665
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                Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Methods and nucleic acids for the analysis of hematopoietic cell proliferative disorders

proliferative disorders

Petent: Mo 02077272-A 45 03-0CT-2002;
                                                                                       Majer,S.

Method and nucleic acids for the analysis of breast cell
proliferative disorders

L. Patent: WO 2004020662-A 50 11-MAR-2004;

Epigenomics AG (DE)
Location/Qualifiers
I. .3025
/organism="Homo sapiens"
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    .3025
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/db_xref="taxon:9606"

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Sequence 45 from Patent WO02077272.
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VERSION KEYWORDS SOURCE ORGANISM

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Pred. No.:

DEFINITION ACCESSION

RESULT 12 AX822116

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.SM Unknown.
Unclassified.
CE 1 (bases 1 to 4086)
XS Emerson, C.P and Goldhamer, D.J.
3 Transcription control element for increasing gene expression in myoblasts
myoblasts
.NAL Patent: US 5681735-A 1 28-OCT-1997;
XES 1. 4086
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                             linear PAT 03-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF027148 12825 bp DNA linear PRI 07-AUG-1998
Homo sapiens myogenic determining factor 3 (MYOD1) gene, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 12825)
Chen,B., Dias,P., Jenkins,J.J. III, Savell,V.H. and Parham,D.M. Methylation alterations of the MyoDl upstream region are predictive of subclassification of human rhabdomyosarcomas
Am. J. Pathol. 152 (4), 1071-1079 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (26-SEP-1997) Pathology, University of Arkansas for
Submitted (26-SEP-1997) Markham St., Little Rock, AR 72205, USP
Medical Sciences, 4301 West Markham St., Little Rock, AR 72205, USP
Methylation alterations in the 5' region are found in embryonal
rhabdomyosarcoma and alveolar rhabdomyosarcoma. Dynamic
methylation changes in this region are found in normal myogenesis.
Location/Qualifiers
                                                                                                                              1761 TACAGCGGCCCCCGAGCGGCGCCCGGCGGAGACTGCTACGAA 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TyrSerGlyProProSerGlyAlaArgArgArgAsnCysTyrGlu 15
                                                                                                     1 TyrSerGlyProProSerGlyAlaArgArgArgArgArgTyrGlu 15
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Sequence 1 from patent US 5681735.
171382
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                                                                                                                                                                                                                                                                                  Adorjan, P., Burger, M., Maier, S., Nimmrich, I., Becker, E., Lesche, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adorjan, P., Burger, M., Maier, S., Nimmrich, I., Becker, E., Lesche, R., Rujan, T. and Schmitt, A.
Rujan, T. and Schmitt, A.
Method and nucleic acids for the analysis of a colon cell
proliferactive disorder
Patent: WO 03072821-A 8 04-SEP-2003;
Epigenomics AG (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAT 11-DEC-2003
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                               Rujan, T. and Schmitt, A. Method and nucleic acids for the analysis of a colon cell proliferative disorder. Patent: EP 1340818-A 8 03-SEP-2003; Epigenomics AG (DE)
     1 TyrSerGlyProProSerGlyAlaArgArgArgAenGyeTyrGlu 15
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Sequence 8 from Patent W003072821.
AX825756
                                                                                                          Sequence 8 from Patent EP1340818. AX822116
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 13

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AX825756

ORGANISM

REFERENCE AUTHORS Bource

Score:

FEATURES

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TITLE

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/product="myogenic determining factor 3"
join (10456. .11065,11555. .11633,11908. .12161)
join (10456. .11065,11555. .11633,11908. .12161)
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RTTWADRRAKATWRERRRLSKVNBAPETLKRCTSSNPNQRLPKVBTLRNATRYTEG
QALLINDQDAAPPGAAAAFYPAGPLPPGGEHYSGDBDASSPRSNCSDGMMDYSGPPS
GARRANCYEGAYYNBAPSEPRPGKSAAVSSLDCLSSTVBRIGTESPAAPALLLADVPS
ESPPRRQEAAAPSEGESSGDPTQSPDAAPQCPAGANPNPTYQVL"
// hote="expressed in early myogenesis and in hote="expressed in early myogenesis and in join(10264. 11065,11555. .11633,11908. .12783) / gene="MYOD1"
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US-10-018-964-3_COPY_1_15 (1-15) x AF027148 (1-12825)

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Search completed: March 7, 2005, 09:09:09 Job time: 1751 secs

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Adp99229 Human tra
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Abz10043 Haematopo
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Abz90108 Human nuc
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                                                                                                                                                                                            ADE84082
ABZ52395
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ADB09169
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AAQ74447
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GENBANK; NM_002478.
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Command line parameters:
-MODEL=frame+pl. model -DEV=xlp
-MODEL=frame+pl. model -DEV=xlp
-Del-cgn2_1/USPTO spool pl/1810018964/runat_03032005_114706_21351/app_query.fasta_1.i99
-DB=N Geneseq_16Dec04_-QPMT=fastap_-SUPFIX_=rng_-MINMATCH=0.1_-LGOPCL=0
-LGOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAR=100 -THR_MIN=0 -ALIGN=15
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-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREAPSIZE=1 CARPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOR=6
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Ada84118 Human MYO
Adq25112 Human sof
Abz09905 Human 5'
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                                                                                                                 6, 2005, 23:13:02 ; Search time 427 Seconds (without alignments) 207.953 Million cell updates/sec
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               GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                   nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                            of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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ADQ25112
ABZ09905
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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geneseqn1980s:*
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seq length: 200000000
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Maximum DB
                                                                                   OM protein
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Database

Result Š.

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Analyzing proliferative diseases of breast cells, useful e.g. for diagnosis, prognosis and treatment of breast cancer, by determining methylation status of specific genes.
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Claim 1; Page; 22pp; German

This invention describes a novel method of analysing proliferative diseases of breast cells by determining the methylation status of certain genes. The invention also describes muclaic acids or their complements, coligomers, especially oligomulectides or peptide nuclaic acids, the class of the invention also describes muclaic acids or their complements, coligomers, especially oligomulectides or peptide nuclaic acids, the preparation of an oligomer array for analysing proliferative diseases of breast cells that are associated with the methylation status of CpG breast cells that are associated with the methylation status of CpG phase and a kit comprising a bisulfite reagent and the oligomer. The process involves a genomic sequence of the oligomer includes at least one control and a bisulfite reagent, to convert non-methylated to the sequence. The crich respicions. The base sequence of the oligomer includes at least one contex base having base-pairing properties different from those of C. with a bisulfite reagent, to convert non-methylated to train some contex base having base-pairing properties different from those of C. crich reagents of the amplitions, pairing properties of different from those of C. creat base having base-pairing properties of the genomic CpG dinucleorides is collymerase and the methylation status of the ypridisation to the oligomer, optionally with extension of the hybridisation to the oligomer, optionally with extension of the hybridisation to the oligomer, optionally with extension of the hybridisation enzymes, from a sample and digested with methylation-specific restriction enzymes, from a sample and digested with methylation-specific primers and a context of the oligomer base, or detection is by sequence of 100-200 by are amplification. In each of the oligomer base, or detection is a pagent of the oligomer base oligomer bas

Sequence 1757 BP; 325 A; 609 C; 540 G; 283 T; 0 U; 0 Other;

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Length:
Matches:
Conservative:
Mismatches:
                                        Indels:
                                                   Gaps:
         87.00
100.00%
100.00%
                              Best Local Similarity:
                    Percent Similarity:
                                         Query Match:
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US-10-018-964-3_COPY_1_15 (1-15) x ADP07312 (1-1757)

ACN39187 standard; cDNA; 1757 BP ACN39187; RESULT 2 ACN39187

ADA84118 standard; DNA; 2480 BP

ADA84118

20-NOV-2003 (first entry)

ADA84118;

SXXXXX

Human MYOD1 gene.

18-NOV-2004 (first entry)

Tumour-associated antigenic target (TAT) cDNA DNA325440, SEQ ID NO:3178. Tumour-associated antigenic target; TAT; human; overexpression; cancer; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe;

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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are coveravpressed in cancer tissues compared to normal tissues, and may thus cavera as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acids and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptide cacids and polypeptides; expression vectors and host cells comprising a TAT nolypeptide; and methods and compositions for the treatment or cacid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; and proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, melsonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with concreased TAT expression, particularly cancers such as breast cancer, increased TAT expression, particularly cancers such as breast cancer, cancer, and cancer, necessions, melsanoma and leukaemia. TAT nucleic acids may further be nervous system, melsanoma and leukaemia. TAT nucleic acids may further be chromosome identification and in gene therapy. The present sequence sequence
                                                                                                                                                                                                                                                                                                                                                                                    New tumor-associated antigenic target polypeptides and nucleic aci
useful in preparing a medicament for treating or detecting a
proliferative disorder, e.g. breast, lung, colorectal, ovarian or
prostate cancer or tumor.
chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1757 BP; 325 A; 609 C; 540 G; 283 T; 0 U; 0 Other;
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 3178; 7273pp; English.
                  gene therapy; cytostatic; gene; ss.
                                                                                                                                                                        29-SEP-2003; 2003WO-US028547.
                                                                                                                                                                                                                 02-OCT-2002; 2002US-0414971P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.00659
87.00
100.00%
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                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                 WPI; 2004-347921/32.
P-PSDB; ABM81235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
                                                                                                                                                                                                                                                                                              Zhang Z,
                                                                                                WO2004030615-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                       15-APR-2004.
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DB:
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26-AUG-2004 (first entry)

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human; marker; expressed sequence tag; EST; arabidopsis; tumour;
stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;
                                                                                                                                                                                                                          Determining if a nucleic acid is a marker for a phenotype/cell type of interest, by global comparison of expressed sequence tags known to be expressed in the phenotype/cell type with all ESTs expressed in normal
                                                                                                                                                                              Kozlov AP, Lobashev AV, Krukovskaya LL;
                                                                                                                               22-OCT-2001; 2001US-0330457P. 19-FEB-2002; 2002US-0357144P.
                                                                                                                      30-MAY-2001; 2001US-0293999P.
                                                                                                    30-MAY-2002; 2002WO-IB004189.
                                                                                                                                                                            Baranova AV, Yankovsky NK,
                                                                                                                                                           (BIOM-) BIOMEDICAL CENT
                                                                                                                                                                                                WPI; 2003-175241/17.
                           vaccine; ds; gene.
                                                                                                                                                                                                        P-PSDB; ADA84119
                                                               WO2002103028-A2.
                                              Homo sapiens
                                                                                 27-DEC-2002
                                                                                                                                                                                                                                                       tissue.
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The invention relates to a novel method for determining if a nucleic acid is a marker for a predetermined phenotype/cell type of interest from a biological species. The method comprises performing a global comparison of a group of expressed sequence tags (ESTS) known to be expressed in the phenotype/cell type of interest with all ESTs expressed in normal tissue in order to identify ESTs that are preferentially expressed in the phenotype/cell of interest. A method of the invention is useful for determining whether a nucleic acid is a marker for a predetermined phenotype or cell type of interest from a biological species, preferably harabidopsis or human. The cell type of interest is an abnormal cell such as a tumour cell, and the predetermined phenotype is a stress-induced beneting the invention is also useful for determining the progression of colon cencer in a human, for detecting a tumour cell, and for regulating or preventing the growth of a tumour cell, an antibody of the invention is useful for detecting the absence or presence of peptides encoded by tumour associated markers. A polypeptide of the invention is useful as an immula. The present sequence encodes a remover associated markers. tumour-associated antigen of the invention Claim 23; Page 498-499; 516pp; English

519 A; 756 C; 725 G; 480 T; 0 U; 0 Other; Sequence 2480 BP;

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2480
115
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       Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
        0.00954
87.00
100.00%
100.00%
                                Best Local Similarity:
                       Percent Similarity
Alignment Scores:
                                     Query Match:
DB:
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US-10-018-964-3_COPY_1_15 (1-15) x ADA84118 (1-2480)

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TACAGCGGCCCCCCGAGCGCCCCGGCGCGGAACTGCTACGAA 894
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1 TyrSerGlyProProSerGlyAlaArgArgArgAsnCysTyrGlu
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ADQ25112 standard; DNA; 2744 BP ADQ25112 ADQ25112

RESULT 4

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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated but the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                          Boft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                numan; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2744 BP; 549 A; 756 C; 740 G; 489 T; 0 U; 210 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human 5' and/or regulatory region of MYOD1 DNA SEQ ID NO:45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     880 TACAGCGGCCCCCCGAGCGGCGCCCGGCGGAACTGCTACGAA 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15
                                     soft tissue sarcoma-upregulated DNA - SEQ ID 7932.
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Matches:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; SEQ ID NO 7932; 210pp; English.
                                                                                                                                                                                                                                                                                                                                                            Zlotnik A;
                                                                                                                                                                                                                                                                                                                       (PROT-) PROTEIN DESIGN LABS INC.
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                                                                                                                                                                                                                                            26-NOV-2003; 2003WO-US038193.
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                                                                                                                                                                                                                                                                                                                                                            Aziz N, Ginsburg WM,
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-441208/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
                                                                                                                                                                    WO2004048938-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                         10-JUN-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barcoma
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Huma
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KW Gene
KW Gene
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Becker E,

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Claim 38; SEQ ID NO 45; 117pp; English.
                               26-MAR-2002; 2002WO-EP003401
                                       26-MAR-2001; 2001US-0278333P
                                                                                                                                                                                                                                                                                                            ADB53952 standard; DNA; 3025
                                                                                                                                                                                                                                                                                                                               (first entry)
                                                 (EPIG-) EPIGENOMICS AG.
                                                                                WPI; 2003-018942/01.
                                                                                                                                                                                                                                                       Similarity:
             WO200277272-A2
                                                                                                                                                                                                                                                  Percent Similarity:
    Homo sapiens
                                                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                              04-DEC-2003
                      03-OCT-2002
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DB:
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The invention relates to a novel method for detecting and differentiating between colon cell proliferative disorders associated with at least one gene or its regulatory regions. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least one reagents or a series of reagents, where the reagent or series of reagents, where the reagent or series of reagents, where the reagent or series of reagents of alternguishes between methylated and non methylated CpG dinucleotides within the target nucleic acid. The method may useful for detecting and differentiating between colon cell proliferative disorders, including cancers such as colon adenome and colon carcinoma. The PNA (peptide nucleic acid)-oligomers are useful as probes for determining cytoshm methylation state or single nucleotide polymorphisms. The current sequence is that of the genomic DNA region of the invention. This sequence is not shown within the specification but is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting and differentiating between colon cell proliferative disorders associated with a gene or its regulatory regions comprises contacting a target nucleic acid in a biological sample obtained from the subject with
                                              colon cell proliferative disorder; non methylated CpG dinucleotide; cytostatic; cancer; adenoma; carcinoma; cytosine methylation state; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; 930 G; 548 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TyrserGlyProProSerGlyAlaArgArgArgAsnCysTyrGlu
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Nimmrich I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 46; SEQ ID NO 8; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Maier S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADE84013 standard; DNA; 3025 BP
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                                                                                                                                                                                                                                                                                    27-FEB-2003; 2003WO-EP002035.
                                                                                                                                                                                                                                                                                                                                     27-FEB-2002; 2002EP-00004551.
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MYOD1 genomic DNA region.
                                                                                                                                                                                                                                                                                                                                                                                         (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                            Burger M,
                                                                                                                                                                                                                                                                                                                                                                                                                 Adorjan P, Bursc. T. Schmitt A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-731620/69.
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                                                                                                                               Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a reagent
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3444444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118 crepresent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative clientating between healthy haematopoietic cells from the present invention acute disorder haematopoietic cells; for differentiating between acute clark and sequences and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polyworphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, disgnosals, prognosals, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables continued to a disorder subclassed and informed treatment of patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
                                                                                                                                                                                                                                                                                                                                                                                      Pelet C;
                                                                                                                                                                                                                                                                                                                             Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J; Olek A, Piepenbrock C, Adorian P, Grabs G, Lesche R, Leu E; Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, 1 Schwope I, Ziebarth H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3025 BP; 535 A; 1012 C; 930 G; 548 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1761 TACAGCGGCCCCCGAGCGGCGCCGGCGGCGGAACTGCTACGAA 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TyrSerGlyProProSerGlyAlaArgArgArgAsnCysTyrGlu 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3025
15
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-018-964-3_COPY_1_15 (1-15) x ABZ09905 (1-3025)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.0118
87.00
100.00%
100.00%
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de; lymphoid cell proliferative disorder; methylation; methylated CpG dinucleotide; single nucleotide polymorphism; SNP;

regulatory region of human gene MYOD1.

(first entry)

29-JAN-2004

15

3025 115 0 0 0

Indels:

Length:

```
The invention relates to a method of detecting and differentiating between lymphoid cell proliferative disorders associated with at least cone gene and/or their regulatory regions in a subject by contacting a target nucleic acid in a biological sample obtained from the subject with car grasper nucleic acid in a biological sample obtained from the subject with car farget nucleic acid in a biological sample obtained from the subject with car grasper nucleic acid. The genes and/or their regulatory regions are preferably selected from MDR1, CSNK2B, EGR4, AR, CDK4, RB2, CDC25A, GPID beta, MYDD1, CDR3B, CKC25A, GPID beta, MYDD1, CDR3B, CKC3FD, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RB2, TGFRR2, TF73, CDKN2B, CGK3FDeta, ESR1, APAF1, BAK, BAX or HOXAS. Oligomers, peptide nucleic acid SKDeta, ESR1, APAF1, BAK, BAX or HOXAS. Oligomers, peptide nucleic acid spaces are useful for detecting the methylation state of all the cyclosine methylation state of all the cyclosine methylation state and or single nucleotide polymorphisms (SNPB), and for differentiating at least two of the medical conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma, chronic lymphoma. They are also useful for detecting of a predisposition to, differentiation between subclasses, diagnosis, prognosis, treating and/or monitoring of lymphoid cell proliferative disorder. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprises contacting a target nucleic acid with at least or
hat distinguishes between methylated and non-methylated CpG
                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting and differentiating between lymphoid cell proliferative
                                                                                                                                                                                                                                                                                                                                              Nimmrich I;
                  chronic lymphocytic leukēmia; small lymphocytic lymphoma;
follicular lymphoma; diagnosis; prognosis.
                                                                                                                                                                                                                                                                                                                                              Maier S,
diffuse large B-cell lymphoma; mantle cell lymphoma;
                                                                                                                                                                                                                                                                                                                                              Becker E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 9; 448pp; English
                                                                                                                                                                                                                                                                                                                                              Genc B,
                                                                                                                                                                                                 25-NOV-2002; 2002WO-EP013265.
                                                                                                                                                                                                                                       23-NOV-2001; 2001DE-01057491.
28-DEC-2001; 2001DE-01064501.
                                                                                                                                                                                                                                                                                                                                            Caldwell C,
                                                                                                                                                                                                                                                                                                    (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-457621/43
                                                                                                                   WO2003044226-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mentioned genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dinucleotides.
                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    that
                                                                                                                                                         30-MAY-2003
                                                                                                                                                                                                                                                                                                                                            Burger M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reagent
```

Sequence 3025 BP; 535 A; 1012 C; 930 G; 548 T; 0 U; 0 Other;

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1761 TACAGCGCCCCCCGAGCGGCGCCCCGGCGGAACTGCTACGAA 1805
                                                                                                                     1 TyrSerGlyProProSerGlyAlaArgArgArgAsnCysTyrGlu 15
                       0 0 0
                                   Conservative:
                                                                                              JS-10-018-964-3_COPY_1_15 (1-15) x ADE84013 (1-3025)
                                               Mismatches:
           Length:
Matches:
                                                           Indels:
                                                                                                                                                                                           AAQ51033 standard; DNA; 4086 BP
          0.0118
87.00
100.00%
100.00%
                                                 Best Local Similarity:
                                  Percent Similarity:
Alignment Scores:
                                                         Query Match:
DB:
                                                                                                                                                                      RESULT 8
                                                                                                                                                                                AAQ51033
ID AAQ
XX
AC AAQ
                                                                                                                                           용
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Human myoD gene and myoblast specific transcriptional control element.
                                         Enhancer; myogenic cells; expression; 5'; control element; antisense oligonucleotides; gene therapy; ss.
                                                                                                                 end of promoter region"
                                                                            Location/Qualifiers
1038. .1044
                                                                                                                                                                                                        (FOXC-) FOX CHASE CANCER CENT
                                                                                                                                                                             93WO-US002767.
                                                                                                                                                                                          92US-00866386.
                                                                                                          /*tag= b
/note= "3' er
1277. .1652
/*tag= c
      (revised)
(first entry)
                                                                                                                                                                                                                       Emerson CP, Goldhamer DJ;
                                                                                             *tag= a
                                                                                                                                                                                                                                    WPI; 1993-351756/44.
P-PSDB; AAR42359.
      25-MAR-2003
09-MAY-1994
                                                                                                                                                                            24-MAR-1993;
                                                                                                                                                                                          10-APR-1992;
                                                               Homo sapiens
                                                                                                                                              WO9321347-A1
                                                                                     TATA_signal
                                                                                                                                                            28-OCT-1993
                                                                                                    promoter
SXCCCCCCCCXXXX141XXBXXBXXBXBXBXI41111111X8XXXXBXXBXXBX
```

Transcription control element with enhancer activity - increases gene expression in myoblast(s) and is derived from upstream region of myob gene.

Claim 1; Page 16-18; 56pp; English.

The sequence is that of the human myob gene and its upstream regulatory sequence. The transcriptional contol element has enhancer activity in myogenic cells, causing increased expression of the myob gene. Antisense oligonuclectide fragments of the control sequence can be used for identifying and locating partic. functional regions in the control element. The myoblast-specific control element will aid advances in gene therapy using myoblast transfer and microinjection techniques. The contol element may also be useful in biochemical assays for the activity of early transcription factors involved in regulating enhancers. See also AAQ51034-5. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 4086 BP; 769 A; 1306 C; 1206 G; 805 T; 0 U; 0 Other;

Length: Matches: Conservative: Mismatches: Indels: 87.00 100.00% 100.00% 0.0163 Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: No.

US-10-018-964-3_COPY_1_15 (1-15) x AAQ51033 (1-4086)

2399 TACAGCGGCCCCCCGAGCGGCGCCCGGCGGAACTGCTACGAA 2443 TyrSerGlyProProSerGlyAlaArgArgArgAsnCysTyrGlu 15 BP. ABZ10043 standard; DNA; 3025 RESULT 9 **AB**Z10043

ABZ10043

AAQ51033

₫B.

```
Haematopoietic cell proliferation disorder related DNA sequence #183
                       Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
                                                                         26-MAR-2002; 2002WO-EP003401.
     16-JAN-2003 (first entry)
                                                      WO200277272-A2.
                                            Homo sapiens
                                                               03-OCT-2002
```

The present introduced a method to discretify and discrete discret Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides. Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J; Olek A, Plepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E; Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C; Schwope I, Ziebarth H; present invention describes a method for detecting and Claim 28; SEQ ID NO 183; 117pp; English 26-MAR-2001; 2001US-0278333P (EPIG-) EPIGENOMICS AG. WPI; 2003-018942/01.

disorders allowing for improved and informed treatment of patients Sequence 3025 BP; 535 A; 245 C; 930 G; 1315 T; 0 U; 0 Other;

Conservative: Mismatches: Indels: Length: Matches: 24.5 64.00 80.00% 80.00% 73.56% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match:

3025 112 0 0 0

TyrserGlyProProserGlyAlaArgArgArgAsnCysTyrGlu 15 US-10-018-964-3_COPY_1_15 (1-15) x ABZ10043 (1-3025)

ADE84081 standard; DNA; 3025 BP

RESULT 11 ADE84081 ID ADE8 XX

The invention relates to a novel method for detecting and differentiating between colon cell proliferative disorders associated with at least one open or its regulatory regions. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least one reagent or a series of reagents, where the reagent with at least one reagent or a series of reagents, where the reagent or series of distinucleotides within the target nucleic acid. The molecules of the invention demonstrate cytostatic activity whilst the method may useful for detecting and differentiating between colon cell proliferative disorders, including cancers such as colon adenoma and colon carcinoma. The PNA (peptide nucleic acid)-oligomers are useful as probes for polymorphisms. The current sequence is that of the pretracted genomic DNA region of the invention. This sequence is not shown within the Detecting and differentiating between colon cell proliferative disorders associated with a gene or its regulatory regions comprises contacting a target nucleic acid in a biological sample obtained from the subject with colon cell proliferative disorder; non methylated CpG dinucleotide; cytostatic; cancer; adenoma; carcinoma; cytosine methylation state; Lesche R; Sequence 3025 BP; 535 A; 245 C; 930 G; 1315 T; 0 U; 0 Other; 1761 rarakcegerrrrceaeceecerreeceeceeceaarrerraceaa 1805 1 TyrserGlyProProSerGlyAlaArgArgArgArgAsGCysTyrGlu 15 Becker E, 3025 12 0 3 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: US-10-018-964-3_COPY_1_15 (1-15) x ADB54091 (1-3025) Maier S, Nimmrich I, specification but is taken from Wipoweb. Claim 32; SEQ ID NO 147; 74pp; English. Pretreated genomic DNA region 15 BP. 27-FEB-2003; 2003WO-EP002035. ADB54091 standard; DNA; 3025 27-FEB-2002; 2002EP-00004551. 24.5 64.00 80.00% 80.00% 73.56% (first entry) (EPIG-) EPIGENOMICS AG Burger M, Adorjan P, Burger M Rujan T, Schmitt A; WPI; 2003-731620/69 Similarity: WO2003072821-A2 Percent Similarity: Unidentified. Alignment Scores: Pred. No.: 04-DEC-2003 04-SEP-2003 reagent ADB54091; Query Match: Local ADB5409 Score: Best ò

09:44:24 2005

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Tue Mar

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Detecting and differentiating between lymphoid cell proliferative disorders comprises contacting a target nucleic acid with at least or reagent that distinguishes between methylated and non-methylated CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nimmrich I;
                                                                                                                  Human lymphoid cell proliferative disorder gene derived DNA #17
                                                                                                                                                                    ds; lymphoid cell proliferative disorder; methylation; methylated CpG dinuclectide; single nuclectide polymorphism; diffuse large B-cell lymphoma; mantle cell lymphoma; chronic lymphorytic leukemia; small lymphocytic lymphoma; follicular lymphoma; diagnosis; prognosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maier S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Becker E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 26; SEQ ID NO 77; 448pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genc B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-NOV-2002; 2002WO-EP013265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-NOV-2001; 2001DE-01057491.
28-DEC-2001; 2001DE-01064501.
                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caldwell C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-457621/43
                                                                                                                                                                                                                                                                                                                                                                                                                WO2003044226-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dinucleotides.
                                                                                                                                                                                                                                                                                                                                                           domo sapiens.
                                                          29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burger M,
ADE84081;
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The invention relates to a method of detecting and differentiating between lymphoid cell proliferative disorders associated with at least cone gene and/or their regulatory regions in a subject by contacting a target nucleic acid in a biological sample obtained from the subject with car least one reagent or series of reagents that distinguish between card lample obtained from the subject with the target nucleic acid. The genes and/or their regulatory regions are preferably selected from MDRI, CSNK2B, EGR4, AR, CDR4, RB2, CDC25A, GPID beta, MYDDI, CDH3, WCLI, EIKI, ABL1, APC, BCL2, CDH1, CDKN1B, CDKN1B, CDKN2B, CDKN2B, FOS, GSTP1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RB12, TGFRR2, TDY3, CDKN1C, CGSTD1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RB2, TGC25A, GPID beta, MYDDI, CDH3, CG GSTD1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RB2, CDC25A, GPID beta, MYDDI, CDH3, CC GSTD1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RB2, TGCN2B, CDKN2B, CDKN2B above mentioned genes.

Sequence 3025 BP; 535 A; 245 C; 930 G; 1315 T; 0 U; 0 Other;

```
3025
12
0
              Matches:
Conservative:
Mismatches:
       Length:
                                       Indels:
      24.5
64.00
80.00%
73.56%
                     Percent Similarity:
Best Local Similarity:
gnment Scores:
                                        Query Match:
```

1 TyrSerGlyProProSerGlyAlaArgArgArgAsnCysTyrGlu 15

```
/ransl except= (pos: 385. .387, aa: Pro)
/transl_except= (pos: 415. .417, aa: Asp)
/transl_except= (pos: 421. .423, aa: Asp)
/transl_except= (pos: 454. .456, aa: Asp)
/transl_except= (pos: 667. .669, aa: Asp)
/product= "transcription factor protein MyoD1"
                                                                                           cDNA sequence encoding the transcription factor protein MyoD1.
1761 TATAGCGGTTTTTCGAGCGGCGTTCGGCGGCGGAATTGTTACGAA 1805
                                                                                                           Transcription factor; MyoD1; myoD1 gene; regulatory gene; skeletal myogenesis; DNA-binding protein; bHLH domain;
                                                                                                                                                                                                                                                                                                                                                                    Almond BD;
                                                                                                                                                                                                                                                                                                                                                                    De Berg LG,
                                                                                                                                                             Location/Qualifiers
                                          BP.
                                          AAA47075 standard; cDNA; 957
                                                                                                                                                                                                                                                                                 99WO-US030460
                                                                                                                                                                                                                                                                                                 98US-0113261P
                                                                                                                                                                                                                                                                                                                                                                    Schenborn ET, Brondyk W,
                                                                           (first entry)
                                                                                                                                                                     ...957
*tag=
                                                                                                                                                                                                                                                                                                                (PROM-) PROMEGA CORP.
(SCHE/) SCHENBORN E T.
(BRON/) BRONDYK W.
(DBER/) DE BERG L G.
                                                                                                                           augmentor sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-442694/38.
                                                                                                                                                                                                                                                                                                                                                   ALMOND B D.
                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAY93769
                                                                                                                                                                                                                                                40200037682-A1.
                                                                                                                                                                                                                                                                                 20-DEC-1999;
                                                                                                                                                                                                                                                                                                 21-DEC-1998;
                                                                           03-OCT-2000
                                                                                                                                                                                                                                                                29-JUN-2000
                                                           AAA47075;
                                                                                                                                                                                                                                                                                                                                                   (ALMO/)
                                                                                                                                              g.
                          RESULT 12
                                  AAA47075
ID AAA4
                                                                                                                                                             Key
```

The present sequence encodes a murine the transcription factor protein

MyoD1. It is derived from the myoD1 gene, which is a regulatory gene for
skeletal myogenesis. The protein is a DNA-binding protein that binds to
the enhancer elements of several muscle-specific genes. The myoD1 gene
contains a bHill domain, which consists of a basic segment that binds to a
consensus DNA sequence (CANNTG) element termed the "E-box", and a short
consensus DNA sequence (CANNTG) element termed the "E-box", and a short
consensus DNA sequence (CANNTG) element termed the "E-box", and a short
consensus DNA sequence (CANNTG) element termed the "E-box", and a short
consensus DNA sequence (CANNTG) element termed the "E-box", and a short
calpha helix connected by a loop to a longer alpha helix. The loop is
cleaved the second polypeptide can be the same or different, and the
colypeptide. The second polypeptide can be the same or different, and the
colypeptide. The sequence can be derived from the myoD1 cDNA
c genes. An augmentor sequence can be derived from the myoD1 cDNA
c sequence, which augments post-transfection expression of a foreign gene
column the myoD1 cDNA in the myoD1 cDNA
c sequence, which augmenter sequence is used in the method of the sequence, which augments post-transfection expression of a cof interest. The augmentor sequence is used in the method invention, for the improving transient gene expression of extrachromosomal foreign gene in a host cell Disclosure, Fig 1A; 133pp; English.

Improving transient expression of an extrachromosomal foreign gene in cultured eukaryotic cells to produce large amounts of a transgenic gene product in cultured cells.

Sequence 957 BP; 182 A; 341 C; 282 G; 152 T; 0 U; 0 Other;

Sequence 1849 BP; 376 A; 584 C; 506 G; 383 T; 0 U; 0 Other;

Matches: Conservative: Mismatches:

20.1 63.00 86.67% 73.33%

Percent Similarity: Best Local Similarity:

Query Match:

Alignment Scores: Pred. No.:

Score:

Indels:

Length:

BP.

AAQ74447 standard; DNA; 3636

RESULT 14

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US-10-018-964-3_COPY_1_15 (1-15) x ACC47992 (1-1849)

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Page

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Cell differentiation; gene expression; neuroprotective; immunomodulator; dermatological; nootropic; antiparkinsonian; antianemic; cytostatic; anti-HIV; protozoacide; vulnerary; deacetylase; MyoD; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enhancing progenitor cell differentiation and regeneration or
differentiation-related gene expression in a progenitor cell, useful for
treating tissue degeneration, comprises contacting the cell with a
deacetylase inhibitor.
                                                                                                                      634 TACAGCGCCCCCCAAGCGGCCCCCGGCGGAGAATGGCTACGAC 678
                                                                                                         1 TyrSerGlyProProSerGlyAlaArgArgArgArgAgnCysTyrGlu 15
          957
111
2
2
0
0
                              Conservative:
Mismatches:
Indels:
                                                                                  JS-10-018-964-3_COPY_1_1S (1-15) x AAA47075 (1-957)
           Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                            (SALK ) SALK INST BIOLOGICAL STUDIES. (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 69-70; 79pp, English.
                                                                                                                                                                        ACC47992 standard; DNA; 1849 BP
                                                                                                                                                                                                                                       Mouse MyoD nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                        17-OCT-2002; 2002WO-US033570
                                                                                                                                                                                                                                                                                                                                                                                            18-OCT-2001; 2001US-0335705P.
25-OCT-2001; 2001US-0343854P.
                              86.67%
73.33%
72.41%
                                                                                                                                                                                                                    (first entry)
          9.92
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sartorelli V, Puri PL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-430347/40.
                                          Similarity:
                                                                                                                                                                                                                                                                                                                             WO2003033678-A2.
                              Percent Similarity:
                                                                                                                                                                                                                    11-AUG-2003
                                                                                                                                                                                                                                                                                                        Mus musculus.
Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                   24-APR-2003.
                                                                                                                                                                                              ACC47992;
                                                     Query Match:
           ..
No.:
                                          Best Local
                                                                                                                                                   RESULT 13
ACC47992
                    Score:
                                                                                                         ò
                                                                                                                              셤
                                                                                                                                                                         C XCCCCCCCCCCCCCCCCCXSXLLLLLXBXLXBXBXLXBXBXAXBXAXBXXBXXBXAXBX
```

MyoD; muscle; gene expression; myoblast; muscle differentiation; rhabdosarcoma cell; nuclear regulatory factor; chemotherapeutic agent; identification; detection; skeletal muscle; ss.

Proximal regulatory region of the MyoD gene.

(first entry)

19-MAY-1995

AAQ74447;

```
The myoD proximal and distal regulatory regions (See AAQ74447, AAQ74448) may be inserted into vectors and used (1) to induce a muscle phenotype in a non-muscle cell; (2) for positive or negative selection of muscle cells (3) for targetted gene expression, specifically in Skeletal muscle, (4) for the expression of genes controlling growth of myoblasts or mutant forms of myoD that modulate muscle differentiation, (5) for engineering rhabdosarcoma cells to increase sensitivity to chemotherapeutic agents, (6) for the expression of growth factors to stimulate skeletal muscle growth in animals, and (7) to identify nuclear regulatory factors that
                                                                                                                                                                                                                                                                                                                                                                             Isolated proximal and distal myoD regulatory regions - and vectors contg. them, for tissue selective gene expression in muscle cells and for positive or negative muscle cell selection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3636 BP; 730 A; 1096 C; 990 G; 814 T; 0 U; 6 Other;
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111
2
2
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                              (HUTC-) HUTCHINSON CANCER RES CENT FRED.
                                                                                                                                                                                                                                                                                                                          Weintraub HM;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 1; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bind to the regulatory region
                                                                                                                                                                                                                                       91US-00753520.
                                                                                                                                                                                                                                                                   91US-00753520.
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73.33%
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                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-316186/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                       03-SEP-1991;
                                                                                                                                                                                                                                                                  03-SEP-1991;
                                                                                                                                                                                                           04-OCT-1994.
                                                                                                                                                                                US5352595-A.
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Pred. No.:
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DB:
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differentiation related gene expression in a progenitor cell. The method involves contacting an undifferentiated progenitor cell. The method involves contacting an undifferentiated progenitor cell with an amount of a deacetylase inhibitor for a period of time sufficient to induce progenitor cell differentiation or enhance expression of the genes. The method is useful in promoting cell differentiation and regeneration using deacetylase inhibitors. The method is used to inhibit, prevent or treat diseases or conditions associated with a degeneration or loss of tissue, court as muscle tissue, nerve tissue or haematopoietic tissue. In particular, the disease or condition is muscular atrophy, muscular cachexia, dermatomyositis Alzheimer's disease, olivopentocerebellar atrophy, hepatocerebral degeneration of nervous tissue, ocular atrophy, hepatocerebral degeneration, idiopathic olivopentocerebral as secondary aplastic anemia, amyotrophic lateral selenosis, poliomyelitis, bone marrow loss induced by radiation therapy or chemotherapy, multiple myeloma, acute lymphocytic leukemia, HIV or trauma. The present sequence represents a mouse MyoD DNA (GenBank Accession No. XM_124916)

The invention relates to enhancing progenitor cell differentiation or

1 TyrSerGlyProProSerGlyAlaArgArgArgAsnCysTyrGlu 15

2000

Conservative: Mismatches: Indels:

80.00% 66.67% 64.37%

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US-10-018-964-3_COPY_1_15 (1-15) x ABZ10044 (1-3025)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of hamatopoletic cell proliferative disorders. The present method enables a highly specific classification of hamatopoletic cell proliferative disorders allowing for improved and informed treatment of patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
Schwope I, Ziebarth H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haematopoietic cell proliferation disorder related DNA sequence #184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
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                                                                         US-10-018-964-3_COPY_1_1S (1-15) x AAQ74447 (1-3636)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 28; SEQ ID NO 184; 117pp; English
                                                                                                                                                                                                                                                                                                                ABZ10044 standard; DNA; 3025 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-JAN-2003 (first entry)
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                                                                                                                                                                                                                                  RESULT 15
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3025

Length: Matches:

349

Alignment Scores: Pred. No.: Score:

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Scoring table:

Searched:

Title: Perfect score:

Sequence:

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Run on:

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Sequence 55, Appli
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Sequence 1007, Ap
Sequence 1007, Ap
Sequence 15832, A
Sequence 186, App
Sequence 7412, Ap
Sequence 5, Appli
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Sequence 11, Appli
Sequence 713, App
Sequence 827, App
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Sequence 3, Appli
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; Sequence 10. 5681735 | O| D| | O|
; Patent No. 5681735 | O| D| O|
; Patent No. 5681735 | O| D|
; Patent No. 5681735 | O| D|
; Patent No. 5681735 | O| D|
; TITLE OF INVENTION: Transcription Control Element for TITLE OF INVENTION: Increasing Gene Expression in Myoblasts NUMBER OF SEQUENCES: 3 | CORRESPONDENCE ADDRESS: | ADDRESSEE: Dann, Dorfman, Herrell and Skillman STREET: 1601 Market Street, Suite 720 | CITY: Philadelphia | STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: ENOPPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,181
FILING DATE: 07-0CT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet B.
REGISTRATION NUMBER: B.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEFONE: (215) 563-4100
TELEFAN: (215) 563-4100
TELEFAN: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1:
                      US-09-902-540-9457

US-09-902-540-1007

US-09-902-540-1007

US-08-470-179-186

US-09-902-540-7412

US-09-902-540-7412

US-09-928-589-1

US-08-427-497E-4

US-08-427-497E-4

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US-08-427-497E-1

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  19103
     Sequence 1, Appli
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Sequence 2087, Ap
Sequence 1803, Ap
Sequence 6289, Ap
Sequence 4534, Ap
Sequence 4534, Ap
Sequence 285, App
Sequence 385, App
Sequence 3430, Ap
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                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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11. /cgn2_6/ptOdata/1/ina/5A_COMB.seq:*
22. /cgn2_6/ptOdata/1/ina/5B_COMB.seq:*
33. /cgn2_6/ptOdata/1/ina/6A_COMB.seq:*
43. /cgn2_6/ptOdata/1/ina/6B_COMB.seq:*
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65. /cgn2_6/ptOdata/1/ina/PCTUS_COMB.seq:*
                           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                   - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-313-181-1
PCT-US94-12912-1
US-07-753-520B-1
US-09-252-991A-2087
US-09-252-991A-1803
US-09-252-991A-1876
US-09-489-039A-6289
US-09-902-540-4534
US-09-902-540-4334
US-09-902-540-1031
US-09-902-540-US-09-002-540-US-09-002-540-US-09-002-540-US-09-002-540-US-09-002-540-US-09-002-540-US-09-002-540-1162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1202784 seqs, 818138359 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                       US-10-018-964-3_COPY_1_15
87
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                               1 YSGPPSGARRRNCYE 15
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Maximum DB seq length: 2000000000
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Match Length DB
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Database :

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Result

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 9012
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: TRANSDUCTION OF CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: c/o Robbins, Berliner & Carson
STREET: 201 North Figueroa Street, Fifth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Spitals, John P.
REGISTRATION NUMBER: 29,215
REFERENCE/DOCKET NUMBER: 1920-341
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 977-1001
              TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (213) 977-1001
TELEFAX: (213) 977-1003
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1785 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                  0.00191
87.00
100.00$
100.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.67%
73.33%
72.41%
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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Best Local Similarity:
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MOLECULE TYPE:
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                                                                                                                            US-08-313-181-1
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Sequence 2087, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: genomic DNA
DESCRIPTION: myoD Genomic; proximal regulatory region myoD gene; Figures 1A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2133 TACAGCGCCCCCCAAGCGGCCCCCGGCGGCAGAATGGCTACGAC 2177
193 TACAGCGCCCCCAAGCGGCCCCCGGCGGCAGAATGGCTACGAC 837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 19910903
CLASSIFICATION: 435
PRIOR APPLICATION UDATA:
APPLICATION UNMBER: none
FILING DATE: none
ATTORNEY/AGENT INFORMATION:
NAME: Sundemo, John, S.
REGISTRATION NUMBER: 74,446
REPERENCE/DOCKET NUMBER: FHCR-1-5789
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 1.206-682-8100; 1-206-224-0727 (direct)
TELEFAX: 1.206-6224-0779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-018-964-3_COPY_1_15 (1-15) x US-07-753-520B-1 (1-3636)
                                                                                            Sequence 1, Application US/07753520B
Patent No. 535295
Patent No. 535295
GENERAL INFORMATION:
APPLICANT: Tapscott, J., Weintraub, H.M., Palmer, T.D.
TITLE OF INVANTION: "MyoD REGULATORY REGION"
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Ki
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.2Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                           STREET: 2800 Pacific First Center, 14
STATE: Washington
COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2M
COMPUTER: IBM PC/386 Compatible
OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: Word for Windows-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/753,520B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 1-206-224-0779
TELEX: 4938023
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3636 base pairs
TYPE: NUCLEIC ACID
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63.00
86.67%
73.33%
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Best Local Similarity:
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Sequence 6289, Application US/09489039A
Sequence 6289, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUMBER: US/09/489, 039A
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 6289
LENGTH: 303
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Patent No. 6833477
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Misegand, Mysococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US/09/902,540
PRIOR APPLICATION NUMBER: 60/217,883
                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-018-964-3_COPY_1_1S (1-15) x US-09-252-991A-1876 (1-1272)
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                                                                                                                                                                                                                                                                                     1272
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Matches:
Conservative:
Mismatches:
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Conservative:
Mismatches:
Indels:
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                    US 60/074,788
                                                                                                                                                                       TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                PRIOR APPLICATION NUMBER: US 60, PRIOR PILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60, PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142; SEQ ID NO 1876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Klebsiella pneumoniae
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52.00
90.91%
72.73%
59.77%
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51.00
81.82%
81.82%
58.62%
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Best Local Similarity:
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Sequence 1803, Application US/09252991A

Sequence 1803, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,190

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 987
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APPLICANT: MARC J Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

PILE REPERBENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18
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Matches:
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                             PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 432
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1876, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                         TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Pseudomonas aeruginosa
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52.00
90.91%
72.73%
59.77%
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52.00
90.91%
72.73%
59.77%
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Best Local Similarity:
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Best Local Similarity:
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DB:
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US-09-902-540-1031/c

| Sequence 1031, Application US/09902540 |
| Patent No. 6833447 |
| GENERAL INFORMATION: |
| APPLICANT: Goldman, Barry S. |
| APPLICANT: Gladman, Barry S. |
| APPLICANT: Stater, Steven C. |
| APPLICANT: Wiegand, Roger C. |
| TITLE OF INVENTION: Wayxococus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(18849)B |
| FILE REFERENCE: 38-10(18849)B |
| CURRENT APPLICATION NUMBER: US/09/902,540 |
| PRIOR APPLICATION NUMBER: 60/217,883 |
| NUMBER OF SEQ ID NOS: 16825 |
| SEQ ID NO 1031 |
| LENGTH: 10835 |
| CURRENT HORSE |
| CONTRACT |
| CO
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Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: EATHWAY GENE EXPRESSION
CORRESPONDENCES: 1490
CORRESPONDENCES: 1490
CORRESPONDENCES: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
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Matches:
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                                                                                                                                                                                                                                                                                                                   Length:
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PRIOR FILING DATE: 2000-07-10
                                                                                                                                 ; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-4534
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51.00
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58.62%
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                                                                                                                                                                                                                                                                                                            180
51.00
76.92%
61.54%
58.62%
                                      NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 4534
LENGTH: 1656
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CALIFORNIA
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Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
Query Match:
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Pred. No.:
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Pred. No.:
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US-09-016-434-285
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No. .
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WS-09-902-540-3430/c

Sequence 3430, Application US/09902540

Patent No. 6833447

GENERAL INFORMATION:

APPLICANT: Hinkle, Gregory J.

APPLICANT: Miegand, Roger C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Waxococcus xanthus Genome Sequences and Uses Thereof FILE REPERENCE: 38-10(15849)B

CURRENT FILING DATE: 2001-07-10

PRIOR PILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

RRIOR FILING DATE: 2000-07-10

SEQ ID NOS: 16825

LENGTH: 783
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ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
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Matches:
Conservative:
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APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.,
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 9A-0002 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 1D NO: 285:
SEQUENCE CHARACTERISTICS:
LENGTH: 202 base pairs
TYPE: nucleic acid
TYPE: strangeness: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Myxococcus xanthus
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CLONE: 1723064
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Query Match:
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Pred. No.:
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Pred. No.:
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GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Stewen C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10 (15849)B
FILE REFERENCE: 38-10 (15849)B
CURRENT APPLICATION NUMBER: U6/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinchel, Gregory J.
APPLICANT: Hinchel, Gregory J.
APPLICANT: Hinchel, Gregory J.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10 (15849)B
CURRENT FILING DATE: 2001-07-10
CURRENT FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 9457
LENGTH: 1449
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Matches:
Conservative:
Mismatches:
                                          Conservative:
Mismatches:
Indels:
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US-09-902-540-9457/c
Sequence 9457, Application US/09902540
; Patent No. 6833447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CRGANISM: Myxococcus xanthus
US-09-902-540-9457
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CRGANISM: Myxococcus xanthus
US-09-902-540-1007
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| Sequence 4090, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craiq et al.
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WINBER: US/09/949,016
| CURRENT APPLICATION NUMBER: 60/241,755
| PRIOR FILING DATE: 2000-04-03
| PRIOR PLICATION NUMBER: 60/231,768
| PRIOR PLICATION NUMBER: 60/231,498
| PRIOR PLING DATE: 2000-10-03
| PRIOR PLING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SOFTHARE: PESELSOF FOR WINDOWS VERSION 4.0
| SEG ID NO 4090
| LENGTH: 1348
                                                                                                                                                                                                                                                                                                              RESULT 12
US-09-902-540-1162
| Sequence 1162, Application US/09902540
| Patent No. 6833447
| GENERAL INFORMATION:
| APPLICANT: Goldman, Berry S. APPLICANT: Goldman, Regory J. APPLICANT: Slater, Steven C. APPLICANT: Slater, Steven C. APPLICANT: Slater, Steven C. TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
| CURRENT FILING DATE: 2001-07-10
| PRIOR PPLICATION NUMBER: US/09/902,540
| CURRENT FILING DATE: 2000-07-10
| PRIOR PPLICATION NUMBER: 60/217,883
| PRIOR PLICATION NUMBER: 60/217,883
| SENGY APPLICATION NUMBER: Solo-07-10
| PRIOR APPLICATION NUMBER: Solo-07-10
| RENGY APPLICA
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Matches:
Conservative:
Mismatches:
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Indels:
Gaps:
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100.00$
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57.47%
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Best Local Similarity:
Query Match:
DB:
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; ORGANISM: Human
US-09-949-016-4090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
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Pred. No.:
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Pred. No.:
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Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0 Percent Similarity: 100.00% Best Local Similarity: 100.00% Query Match: 56.32% DB:

US-10-018-964-3_COPY_1_15 (1-15) x US-09-902-540-1007 (1-13466)

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Search completed: March 7, 2005, 10:06:20 Job time : 134 secs

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; Search time 163 Seconds
(without alignments)
35.591 Million cell updates/sec
GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	SUMMARIES	Description	ADA84119 Ada84119 Human MYO	ABM81235 Tumour-as		Human	ABP62934 Human pol		AAU49323 Aau49323 Propionib	ABM45842 Abm45842 Propionib	ABO61345 Klebsiell	ABU34694 Abu34694 Protein e	ABU36648 Protein e	ADD24621 DNA polym	AAU52239 Aau52239 Propionib	ABM48758 Propionib		AAY74328 Aay74328 Neisseria	ABO77466 Pseudomon	Adq19641		AAY90927 Cenarchae	ABRS4306 Auman sec	ABO76047 Abo76047 Pseudomon	AAY52590 Human pro	Novel	
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Aam78292 Human bon	Aam65669 Human bra	Abr40491 Human sec	Abr40417 Human sec	Aael1965 Zea mays	Abo69382 Pseudomon	Aaw71561 Human hep	Abm83171 Human dia	Abm83170 Human dia	Abb64915 Drosophil	Abg01164 Novel hum	Abo73678 Pseudomon	Abo70184 Pseudomon	Abg14126 Novel hum	Abo57042 Human gen	Aau64841 Propionib	Aau67196 Propionib	Abm63715 Propionib	Abm61360 Propionib	Aau44993 Propionib
AAM78292	AAM65669	ABR40491	ABR40417	AAE11965	AB069382	AAW71561	ABM83171	ABM83170	ABB64915	ABG01164	AB073678	ABO70184	ABG14126	ABO57042	AAU64841	AAU67196	ABM63715	ABM61360	AAU44993
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48.3	48.3	48.3	48.3	48.3	48.3	48.3	48.3	48.3	48.3	48.3	48.3	48.3	47.7	47.1	47.1	47.1	47.1	47.1	47.1
42	42	42	42	42	42	42	42	42	42	42	42	42	41.5	41	41	41	41	41	41
56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

human, marker; expressed sequence tag; BST; arabidopsis; tumour; stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen; Determining if a nucleic acid is a marker for a phenotype/cell type of interest, by global comparison of expressed sequence tags known to be expressed in the phenotype/cell type with all BSTs expressed in normal Krukovskaya LL; Kozlov AP, Lobashev AV, ADA84119 standard; protein; 320 AA 30-MAY-2001; 2001US-0293999P. 22-OCT-2001; 2001US-0330457P. 19-FEB-2002; 2002US-0357144P. 30-MAY-2002; 2002WO-IB004189. Baranova AV, Yankovsky NK, entry) (BIOM-) BIOMEDICAL CENT. WPI; 2003-175241/17. (first Human MYOD1 protein. N-PSDB; ADA84118. WO2002103028-A2. Homo sapiens. 20-NOV-2003 27-DEC-2002. ADA84119; vaccine. tissue. RESULT 1 ADA84119

Claim 29; Page 499-501; 516pp; English.

The invention relates to a novel method for determining if a nucleic acid is a marker for a predetermined phenotype/cell type of interest from a biological species. The method comprises performing a global comparison of a group of expressed sequence tags (ESTS) known to be expressed in the phenotype/cell type of interest with all ESTs expressed in normal tissue in order to identify ESTs that are preferentially expressed in the phenotype/cell of interest. A method of the invention is useful for determining whether a nucleic acid is a marker for a predetermined

molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers used as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, covarian cancer, liver cancer, bladder cancer, pancreatic cancer, covarian cancer, cancers of the central used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT polypeptide of the invention

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Gaps

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Length 320;

100.0%; Score 87; DB 8; Length 32 100.0%; Pred. No. 0.0001; .ive 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.
Matches 15; Conservative

Sequence 320 AA;

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phenotype or cell type of interest from a biological species, preferably Arabidopsis or human. The cell type of interest is an abnormal cell such as a tumour cell, and the predetermined phenotype is a stress-induced phenotype such as hyperosmotic stress or high salt conditions. A method of the invention is also useful for determining the progression of colon cancer in a human, for detecting a tumour cell, and for regulating or preventing the growth of a tumour cell. An antibody of the invention is useful for detecting the absence or presence of peptides encoded by immunogen for vaccinating an animal. The present sequence represents a number associated antigen of the invention is useful as an tumour-associated antigen of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour-associated antigenic target (TAT) polypeptide PRO81964, SEQ:3179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumour-associated antigenic target; TAT; human; overexpression; cancer; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
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Pred. No. 0.0001;
; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 15, Conservative
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                                                                                                                                                                                     Sequence 320 AA;
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ABM81235
   8×66666666668×8
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Amino acid sequence of the transcription factor protein MyoD1.
                                                                                                                                                                                                                                                        (02. .121
note= "basic domain involved in myogenesis"
                                                                                                                              Transcription factor; MyoDl; myoDl gene; regulatory gene; skeletal myogenesis; DNA-binding protein; bHLH domain; augmentor sequence.
                                                                                                                                                                                                  . .53 "note= "transcription activation domain"
                                                                                                                                                                                                                                                "nuclear localisation signal"
                                                                                                                                                                                                                                                                                                                  .30. .135
note= "nuclear localisation signal"
                                                                                                                                                                                                                                                                                                                                                                                     AAC"
                                                                                                                                                                                                                                                                                                                                                                                                                         note= "Asp encoded by AAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Asp encoded by AAT"
                                                                                                                                                                                                                                                                                                         note= "Pro encoded by TTC"
                                                                                                                                                                                                                                                                                                                                                                   note= "Asp encoded by AAC"
                                                                                                                                                                                                                                                                                                                                                                                    'note= "Asp encoded by
                                                                                                                                                                                                                             'note= "acidic domain"
                                                                                                                                                                                                                                                                                                                                                                                                       'note= "second helix"
                                                                                                                                                                                                                                                                            .22. .136
note= "first helix"
                                                                                                                                                                                                                                                                                                                                               note= "loop region"
                                                                                                                                                                                       Location/Qualifiers
                                                    AAY93769 standard, protein; 318 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US030460.
213 YSGPPSGARRRNCYE 227
                                                                                           03-OCT-2000 (first entry)
                                                                                                                                                                                                                                       .112
                                                                                                                                                                                                                                                                                                                                      137. .145
                                                                                                                                                                                                                   .47
                                                                                                                                                                                                                                                  note=
                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-DEC-1999;
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                                                                        AAY93769;
                                                                                                                                                                      ds snw
                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                      Domain
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                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                          Key
                                    RESULT 3
                                            AAY93769
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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acid and polypeptide polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic

tumor-associated antigenic target polypeptides and nucleic acids,

Wu TD, Zhang Z, Zhou Y;

WPI; 2004-347921/32. N-PSDB; ACN39187

(GETH) GENENTECH INC.

useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or

Claim 12; SEQ ID NO 3179; 7273pp; English.

prostate cancer or tumor.

(PROM-) (SCHE/)

(BRON/) (DBER/) (ALMO/)

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The nucleotide sequence encoding this protein was used to design a large number of antisense oligonucleotides which are targeted to nucleic acids encoding fra-1. The sequences may be oligodeoxyribonucleotides or chimeric oligonucleotides containing a central gap region consisting of ten 2'-deoxynucleotides, which is flanked on both sides by 2'-methoxyethyl (2'-WOE) wings. The oligonucleotides have a phosphorothicate backbone and the cytidine residues in the 2'-MOE wings are 5-methylcytidines. The fra-1 antisense oligonucleotides are useful for inhibiting the expression of fra-1 in human cells or tissues. They can be used for diagnostics, therapeutics, prophylaxis and as research reagents and in kits. Use of the antisense compounds may also be useful tumour formation
                                                                                                         Novel antisense compound 8-30 nucleobases in length targeted to human fra -1 and which specifically hybridizes with and inhibits the expression of human fra-1, useful for modulating the expression of fra-1 in cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, vulnerary; dermatological; neuroprotective; nootropic; cancer; antiparkinsonian; immunostimulant; cytostatic; immunosuppressive; antidiabetic; antiallergic; gene therapy; wound healing; tissue repair; burn; central nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; immune disorder; autoimmune disorder; multiple sclerosis; diabetes; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide and polypeptides, useful for treatment and diagnosis of Alzheimer's, Parkinson's, Huntington's, amylotrophic lateral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang J, Wang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YI, Agundi V, Zhou P, Xue AJ, Ren F, Zhai
Zhao QA, Wang D, Liu C, Drmanac RT, Wehrman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47; DB 3
Pred. No. 76;
0; Mismatches
                                                                                                                                                                                             Disclosure; Col 43-46; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP62934 standard; protein; 271 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-AUG-2001; 2001WO-US027093.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPPSGARRRNC 13
Cowsert LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
8; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPPPGVRRRPC
                                      WPI; 2000-601552/57.
N-PSDB; AAC60503.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABQ93413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 271 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200218424-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-MAR-2002
Taylor JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP62934;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           요
                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a murine the transcription factor protein MyoD1. It is derived from the myoD1 gene, which is a regulatory gene for skaletal myogenesis. The protein is a DNA-binding protein that binds to the enhancer elements of several muscle-specific genes. The myoD1 gene contains a bHLH domain, which consists of a basic segment that binds to alpha helix connected by a loop to a longer alpha helix. The loop is flaxible and allows the two helices to fold back against each other. The alpha helix bids to DNA and the HLH structure of another bHLH connected by a loop to a longer alpha helix. The loop is clexible and allows the two helices to fold back against each other. The alpha helix bids to DNA and the HLH structure of another bHLH cresulting protein complexes then bind to DNA in the 5' regulatory regions of genes. An augmentor sequence can be derived from the myoD1 cDNA sequence, which augments post-transfection expression of a foreign gene cinvention, for the improving transient gene expression of an extrachromosomal foreign gene in a host cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                    Improving transient expression of an extrachromosomal foreign gene in cultured eukaryotic cells to produce large amounts of a transgenic gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; fra-1; antisense oligonucleotide; phosphorothioate; cytostatic; antiinflammatory; 2'-methoxyethyl wing; 2'-MOB wing; infection; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                             De Berg LG, Almond BD;
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; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1B; 133pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                  98US-0113261P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-00418641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YSGPPSGARRRNCYE 15
                                                                                                                                                                                                                                                                                                                                                  product in cultured cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 66.7
nes 10; Conservative
                                                                                                                                                                                           Schenborn ET, Brondyk
                                                                             SCHENBORN E T.
BRONDYK W.
DE BERG L G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ISIS-) ISIS PHARM INC
                                                           PROMEGA CORP.
                                                                                                                                                                                                                                         WPI; 2000-442694/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human fra-1 protein
                                                                                                                                               ALMOND B D.
                                                                                                                                                                                                                                                             N-PSDB; AAA47075.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 318 AA;
               21-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-OCT-1999;
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Query Match

Matches

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AAB28444;

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Gaps

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called prostate cancer antigens, given in AAB56363 to AAB57302
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                                                                                                                                                                                                                                                                                   invention
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                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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              셤
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                                                                                                  The invention relates to an isolated polynucleotide (I) comprising one of 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising cadministering to a mammalian subject a composition comprising the protein (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).

(I) is useful for gene therapy of diseases and (II) can be used for therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's, Huntington's and amylotrophic lateral sclerosis, diabetes and allergies. Note: The sequence data for this sclerosis, diabetes and allergies. Note: The sequence data for this con nelectronic formmat directly from WIPO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.
immune deficiencies, cancer, autoimmune disorders, multiple diabetes and allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human prostate cancer antigen protein sequence SEQ ID NO:968.
                                                            SEQ ID NO 371; 284pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.0%; Score 47; DB 5; Length 271; 72.7%; Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 72.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GPPSGARRRNC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 GPPPGVRRRPC 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-587513/55.
N-PSDB; AAF15593.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 271 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200055174-A1
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                       sclerosis,
                                                            Claim 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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AAB56390

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The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnosite of research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative habbility and infectious diseases. AAPI6506 to AAPI6514 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                       Gарв
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                                                                                                                                                                                                                                                                                                                         Score 47; DB 3; Length 291;
Pred. No. 81;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Propionibacterium acnes immunogenic protein #10219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitcham JL, Wang Si
Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; SEQ ID NO 10518; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU49323 Btandard; protein; 54 AA.
                                                                                                                                                                                                                                                                                                                       54.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-APR-2001; 2001WO-US012865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Skeiky YAW, Persing DH, M.
L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           107 GPPPGVRRRPC 117
                                                                                                                                                                                                                                                                                                                                                                                                      3 GPPSGARRRNC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-616774/71.
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                             Sequence 291 AA;
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Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders

AAF15566 to AAF16505 encode the human prostate cancer associated

Claim 11; Page 1408-1409; 2338pp; English.

antigens, useful ror tresuch as prostate cancer.

polynucleotides, antibodies, fusion proteins, T cell populations,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding a Propionibacterium acres protein. The invention also relates to polypeptides encoded by the polynuclectides (ABM35624-ABM64536) and to immunogenic fragments of P. acres polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polynuclectide of the invention; antibodies against polypeptides of the invention; invention; fusion proteins comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acres polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acres polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Propionibacterium acnes polypeptides and polynucleotides encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
               presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by existent allowed immunosorbent assay (BLISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maisonneuve JL;
Jones R, Carter D;
                                                                                                                                                                                                                                                                                                                                               Gaps
 lesions associated with acne vulgaris. A method for detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes predicted ORF-encoded polypeptide #10518.
                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                                                                                                                      Score 46; DB 4; Length 54;
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Persing DH, Bhatia A,
Lodes MJ, Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID NO 10518; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunostimulant; immune response; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABM45842 standard; protein; 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang Y, Wang S, Jen S, Lod
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                    52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-OCT-2001; 2001US-00978825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                   3 GPPSGARRRNCY 14
                                                                                                                                                                                                                                                                                                                                                                                                                      2 GPPSCPRRRGCH 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes.
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N-PSDB; ACF64474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003033515-A1.
                                                                                                                                                                                                                                                                    Sequence 54 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABM45842;
                                                                                                                                                                                                                                                                                                                                             Matches
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8888888888888888888888888888888888
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projections and the second of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for
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and kit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant expression vector; transcription regulatory element; Klebsiella pneumoniae protein; antibacterial; Vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABO61345 standard; protein; 117 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 52.9
Best Local Similarity 66.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Osborne M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-895346/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ACH94896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 54 AA;
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid conciding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding to proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway confideration or the activity against a biological pathway in which a proliferation or that inhibits cellular proliferation or the biological pathway identifying a gene required for cellular proliferation or the biological pathway in which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a companied acts; (10) activity; (11) a culture comprising strains in which the gene convoluted is overexpressed or underexpressed; (12) determining the extent of which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the convolution of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids are useful for a companied acids are useful for a companied.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             screening
                                                                                                                                                                                                                                                                                                                                                              Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
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    DB 7; Length 117;
48;
                                          3; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                        Protein encoded by Prokaryotic essential gene #20221.
  Score 46; DB 7
Pred. No. 48;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; SEQ ID NO 62618; 1766pp; English.
                                                                                                                                                                                                           ABU34694 standard; protein; 1167 AA.
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Carr GJ,
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2001US-0342923P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002US-00072851
                                                                                                                                                                                                                                                                                       (first entry)
                                    8; Conservative
                                                                         2 SGPPSGARRRNC 13
                                                                                               1 SGPRAGGRRRQC 12
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium bovis.
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N-PSDB; ACA38564.
                  Best Local Similarity
Matches 8: Conserv
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25-OCT-2001;
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Query Match
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Wall D,
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for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fitp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid:
encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated antisense capteeside or its fragment whose expression is inhibited by the antisense the polypeptide or its fragment whose expression is inhibited by the polypeptide; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a gene in an operor required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                  Gaps
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid comprising any
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Pred. No. 6e+02;
1; Mismatches 5; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded by Prokaryotic essential gene #22175.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; SEQ ID NO 64572; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        ABU36648 standard; protein; 1184 AA.
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342523P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                        Similarity 57.1%;
8; Conservative
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                                                                                                                                                                                                                                                                                                               334 AGPPDGYRERAAYE 347
                                                                                                                                                                                                                                                                            2 SGPPSGARRRNCYE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Trawick JD,
                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2003-029926/02
                                                                                                                                                                   Sequence 1167 AA;
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Wall D,
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Matches
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identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed, (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for callular proliferation to isolate candidate molecules for rational for equired for proliferation in cells other than S. aureus, S. typhimurium, C. K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained for the darget probaryotic formed directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1184 AA;
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51.7%; Score 45; DB 6; Length 1184; 57.1%; Pred. No. 6.1e+02; ive 1; Mismatches 5; Indels
                                                                                                     335 AGPPDGYRERAAYE 348
                                                                       2 SGPPSGARRRNCYE 15
                                       Conservative
                Best Local Similarity
Matches 8; Conserv
 Query Match
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Gaps

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RESULT 12

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ADD24621 standard; protein; 1184 AA.
                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                            ADD24621;
ADD24621

XX
AC
ADD3

XX
ADD4

XX
ADD5

XX
ADD7

AD
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DNA polymerase III replicase; dnaE; holA; holB; holD; holD; dnaX; dnaN; SSB; dnaQ; dnaQ; bacterial DNA replication; bacterial infection. DNA polymerase III subunit related protein, SEQ ID No 140.

Mycobacterium tuberculosis

WO200292769-A2

21-NOV-2002.

14-MAY-2002; 2002WO-US015111

14-MAY-2001; 2001US-0290725P. 05-NOV-2001; 2001US-0332644P.

(REPL-) REPLIDYNE INC

Mchenry CS; Bullard JM, Janjic N,

WPI; 2003-120672/11.

Screening for a compound that modulates the activity of Y. pestis and/or P. aeruginosa DNA polymerase III replicase, useful for reducing bacterial MNA replication and infection in animals, plants, humans and surrounding environment.

Disclosure; SEQ ID NO 140; 388pp; English.

The invention relates to a novel screening method for a compound that modulates the activity of a DNA polymerase III replicase. The novel method comprises contacting an isolated replicase with at least one test compound under conditions permissive for replicase activity, and comparing the activity of the replicase in the presence and absence of the test compound, where a change in the activity of the replicase.

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              replicase comprises an isolated nucleic acid from Yersinia pestis or a beaudomonas aeruginosa encoding a DNA polymerase III subunit protein. The DNA polymerase III subunit proteins include dnas. hol4, hol9, holC, holD, holb, dnaX, dnaN, SSB, dnaG, and dnaQ. The methods and compositions of the present invention are useful for reconstituting replicases and polymerases for sequencing, amplification and screening for compounds which modulate the function of the polymerase or replicase particularly in bacterial DNA replication, thereby reducing bacterial infection in animals, plants, humans and the surrounding environment. This sequence represents a DNA polymerase III subunit related protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
indicates a compound that modulates the activity of the replicase.
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                                                                                                                                                                                                                                                                             Length 1184;
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                                                                                                                                                                                                                                                                         51.7%; Score 45; DB 7; Length 118
57.1%; Pred. No. 6.18+02;
tive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Propionibacterium acnes immunogenic protein #13135.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID NO 13434; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU52239 standard; protein; 70 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
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N-PSDB; AAS59553.
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                                                                                                                                                                                                                                                                                              Local Similarity
hes 8; Conserv
                                                                                                                                                                                                                                      Sequence 1184 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200181581-A2.
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Matches
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The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polyneptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polyneptides. The invention additionally encompasses expression vectors and host cells comprising a polynucleotide of the invention; antibodies against polypeptides of the invention; antibodies against polypeptides of the invention; a polypeptide and an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polymentedes, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Propionibacterium acnes polypeptides and polymucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maisonneuve JL;
Jones R, Carter D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 4; Length 70;
Pred. No. 59;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bhatia A,
Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; SEQ ID NO 13434; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunostimulant; immune response; vaccine
                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
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Zhang Y, Wang S, Jen S, Lodes MJ,
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABM48758 standard; protein; 70 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.6%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-OCT-2002; 2002WO-US032727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-OCT-2001; 2001US-00978825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003033515-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 70 AA;
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ABM48758
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for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; The P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acnes to polypeptides are useful for diagnosing, preventing or treating acnes or ungarish, or for stimulating an immune response specific for a P. acnes protein. The polynucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present a gequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated polynucleotide encoding bone marrow derived polypeptides useful for treating, e.g., Parkinson's, Alzheimer's, cancer, arthritis, Crohn's disease, and inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .109
/label= OTHER
/note= "OTHER= All Xaa's in this sequence are unknown
amino acids or the site of a stop codon within the DNA
sequence"
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunosuppressive; cytostatic; antipsoriatic; antiinflammatory; antibacterial; antivinal; antiingal; antiparasitic; gene therapy; arthritis; Parkinson's; Alzheimer's; autoimmune disease; cancer; psoriasis; inflammatory bowel disease; infection; bacteria; virus;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiarthritic; antiparkinsonian; neuroprotective; nootropic;
                                                                                                                                                                                                                                                                                                                                6; Length 70;
                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                Score 44; DB 6
Pred. No. 59;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADK34673 standard; protein; 109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human polypeptide SegID6755.
                                                                                                                                                                                                                                                                                                                                                                1,
                                                                                                                                                                                                                                                                                                                            50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-MAR-2001; 2001WO-US004941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT, Liu C, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                      8, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      2 SGPPSGARRRN 12
                                                                                                                                                                                                                                                                                                                                                                                                                                          64
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Best Local Similarity
Matches 8, Conserv
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                                                                                                                                                                                                                                                                                              Sequence 70 AA;
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19-MAY-2000;
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This invention relates to a novel isolated polynucleotide comprising a nucleotide sequence selected from one of 1680 sequences, a mature protein coding portion of them, an active domain of them and their complementary sequences. The invention may be useful for the production of compounds with an antiarthritic, antiparkinsonian, neuroprotective, nootropic, immunosuppressive, cytostatic, antipsoriatic, antipsoriatic, antinflammatory, antibacterial, antiviral, antifungal or antiparasitic activity. In addition, the disclosed sequences may be useful for gene therapy. The polypeptides or their antibodies are useful for treating many diseases such as arthritis, parkinson's, Alzhaimer's, autoimmune diseases, cancer, psoriasis, inflammatory bowel disease and infections caused by bacteria, viruses, fungi or parasites. The present sequence is that of a human polypeptide of the invention.

Sequence 109 AA;

Gaps ö 50.6%; Score 44; DB 5; Length 109; 63.6%; Pred. No. 89; 3; Indels tive 1; Mismatches 3; Indels Query Match Best Local Similarity 63.6 Matches 7; Conservative

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Search completed: March 3, 2005, 13:56:27 Job time : 164 secs

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RESULT 2
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21532, A
18183, A
21289, A
25992, A
27955, A
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                                                                                                                                  March 3, 2005, 13:51:16 ; Search time 42 Seconds (without alignments) 26.660 Million cell updates/sec
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-252-991A-26212
US-09-252-991A-24793
US-09-252-991A-24793
US-08-459-448A-19
US-08-459-59A-19
US-08-459-59A-19
US-09-56A-19
US-09-988-462-19
US-09-988-462-19
US-09-988-462-19
US-09-988-462-19
US-09-252-991A-18128
US-09-252-991A-18138
US-09-252-991A-18133
US-09-252-991A-25892
US-09-252-991A-218133
US-09-252-991A-218133
US-09-252-991A-218183
US-09-252-991A-25008
US-09-252-991A-218183
US-09-252-991A-25008
US-09-252-991A-25008
US-09-252-991A-25008
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US-09-252-991A-25008
US-09-854-845-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                            513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                            - protein search, using sw model
                                                                                                                                                                                                                                      US-10-018-964-3_COPY_1_15
87
                                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                 1 YSGPPSGARRRNCYE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
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40.5
                                                                                                                                                                                                                                                             Perfect score:
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                                                                                            OM protein
                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                                       Run on:
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Sequence 26212, Application US/09252991A

Sequence 26212, Application US/09252991A

Sequence 26212, Application US/09252991A

Setent No. 6551795

GENERAL INFORMATION:

APPLICANT:

APPLICANT:

TITLE OF INVENTION:

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION:

TITLE OF INVENTION:

NURBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PLING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 26512

LENGTH: 464
                                                                                                                                                                                                                                                                                                                                                                           Sequence 7862, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: GATY BECON et. al
APPLICANT: GATY BECON et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
RIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                      Sequence 29, Appl
Sequence 27, Appl
Sequence 31, Appl
Sequence 31073, A
Sequence 15677, A
Sequence 29348, A
Sequence 29348, A
Sequence 29348, A
Sequence 29348, A
                                                                                                                                                                                                                                          74, Appl
32308, A
                                                                                                                                                                                                                             25820,
                              Sequence
Sequence
Sequence
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               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.9%; Score 46; DB 4; Length 117; 66.7%; Pred. No. 6.8;
                                                      US-09-854-845-47
US-09-854-845-29
US-09-854-845-31
US-09-854-845-31
US-09-854-845-31
US-09-25-991A-31073
US-09-252-991A-31073
US-09-252-991A-31733
US-09-252-991A-31733
US-09-252-991A-31733
                                                                                                                                                                                                                                          US-09-925-637-74
US-09-252-991A-32308
                                                                                                                                                                                                          US-09-252-991A-25394
US-09-252-991A-25820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 SGPPSGARRRNC 13
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SGPRAGGRRRQC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 8; Conserv
2.04440.5
2.044404440.5
2.0.04400.5
4.005
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APPLICANT: Koziel, Michael G.
APPLICANT: Lewis, Kelly.
APPLICANT: Lewis, Kelly.
APPLICANT: Lewis, Kelly.
APPLICANT: Examer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Wright, Martha S.
APPLICANT: Wright, Martha S.
APPLICANT: Martha S.
APPLICANT: Martha S.
APPLICANT: Martha S.
APPLICANT: Rothatein, Steven J.
APPLICANT: Bowman, Cind, G.
APPLICANT: Bowman, Cind, G.
APPLICANT: Bowman, Cind, G.
APPLICANT: Bowman, Cind, G.
APPLICANT: Budger, Erik M.
APPLICANT: Butte, Janet L.
APPLICANT: Sutte, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ő
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
SOFTWARE:
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION 1992
CLASSIFICATION TO SOFTWARE: US/07/951,715A
FILING DATE: 04-0CT-1991
ATPOINTEY/AGENT INFORMATION:
NAME: SPETILIN W. MULTRAY
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: S-18805/A/CGC 1577/CIP
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: CIBA-GBIGY Corporation 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
8.08-459-448A-19
Sequence 19, Application US/08459448A
Patent No. 5859336
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
                Sequence 19, Application US/07951715A Patent No. 5625136 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 346 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 SGPPSGARRRNCYE 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
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Best Local Similarity
Matches 6; Conserva
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STREET: 7
  US-07-951-715A-19
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US-09-252-991A-24793
; Sequence 24793, Application US/09252991A
; Sequence 24793, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: MATC J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24793
: LENGTH: 258
                                                                                                                                                                                                                                                       Sequence 32, Application US/09408020
| Patent No. 6632937
| Fatent No. 6632937
| GENERAL INFORMATION:
| APPLICANT: Swanson, Rohat A.
| APPLICANT: Schleper, Christa
| TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
| FILE REFERENCE: DCORP. 1059-09-29
| CURRENT APPLICATION NUMBER: 05/102,294
| PRIOR FILING DATE: 1999-09-29
| PRIOR FILING DATE: 1998-09-29
| PRIOR FILING DATE: 1998-09-29
| NUMBER OF SEQ ID NOS: 123
| SOFTWARE: FastSEQ for Windows Version 3.0
| SEQ ID NO 32
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                     DB 4; Length 464;
54;
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                                                                 0; Indels
                50.6%; Score 44; DB 100.0%; Pred. No. 54; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Cenarchaeum symbiosum
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54 YNGTPPGV--KNCYE 66
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Query Match
Best Local Similarity 100.
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Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                                                                       101 GPPSGARR 108
                                                                                                           3 GPPSGARR 10
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US-09-408-020-32
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Gaps

RESULT 5

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APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 346;
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                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: New LOLA
COUNTRY: New LOLA
ZIP: 10591-9005
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Parentin Release #1.0, Version #1.30
SOCTWARE: Parentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,595A
FILING DATE: 02-UNA-1995
CLASSIFICATION APA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-0CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: 40403
REFERENCE/TOCKET NUMBER: CGC 1577/CIP/DIV3
TELEPHONE: (919)541-8582
TELECOMMUNICATION NUMBER: CGC 1577/CIP/DIV3
TELEPHONE: (919)541-8582
TELEPHONE: (919)541-8689
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
TENGTH: 346 amino acids
                                                                                                                                                                                                                                                                                                       ADDRESSEE: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 49.4%; Score 43; DB 3; Best Local Similarity 42.9%; Pred. No. 57; Matches 6; Conservative 3; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19, Application US/08459504B
Patent No. 6075185
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Boola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
Rothstein, Steven J.
Bowman, Cindy G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 346 amino acids amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                      CITY: Tarrytown STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-459-595A-19
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US-08-459-504B-19
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                                      APPLICANT: Crossiand, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Wright, Martha S.
APPLICANT: Hearlin, Ellis J.
APPLICANT: Bunnis, Karen L.
APPLICANT: Bowman, Cindy G.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, Cindy G.
APPLICANT: Dawson, Cindy G.
APPLICANT: Suttie, John L.
APPLICANT: Suttie, John L.
APPLICANT: Suttie, John L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                              TOTAL SEQUENCES: 94 CORRESPONDED ACTIVITY IN PALES OF THE SEQUENCES: 94 CORRESPONDENCE ADDRESSS: ADDRESSEE: No. 5859336artis Corporation STREET: Patent & Trademark Dept., 520 White Plains STREET: Rd., POB 2005 CITY: Tarrytown STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-459-595A-19; Sequence 19, Application US/08459595A; Patent No. 6018104; Patent No. 6018104; APPLICANT: Koziel, Michael G.; APPLICANT: Desai, Nalini M.; APPLICANT: Lewis, Kelly S.; APPLICANT: Kramer, Vance C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                      Evola, Stephen V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 346 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 AAPPQAGRRRRCHQ 76
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Best Local Similarity 42.97
Thea 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
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Gaps

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NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:
ADDRESSE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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US-09-547-422-19
US-09-547-422-19
Sequence 19, Application US/09547422

| Patent No. 6320100
| Patent No. 6320100
| GENERAL INFORMATION:
| Lewis, Maini M. |
| Lewis, Rely S. |
| Kramer, Vanen, Gregory W. |
| Bvola, Stephen V. |
| Cossland, Lyle D. |
| Wright, Martha S. |
| Merlin, Blis J. |
| Lawis, Karen L. |
| Lawis Merlin, Blis J. |
| Lawis Merlin, Blis J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gарв
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APPLICATION NUMBER: US/08/459,444A

FILING DATE: 02-Jun-1995

CLASSIFCATION NUMBER: US/08/1,715

FRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/772,027

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 25-SEP-1991

ATTORNEY/AGENT INCORMATION:

NAME: Medigs, J. Timothy

RECISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 19:

SEQUENCE CHARACTERISTICS:
                                                                                                             Wright, Martha s.
Merlin, Ellis J.
Launis, Karen L.
TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUCLEIC ACID CODING SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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42.9%; Pred. No. 57;
tive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 346 amino acids
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Best Local Similarity 42.9
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-459-444-19
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APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Werlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Bowman, Clindy G.
APPLICANT: Bowman, Clindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Dunder, Erik M.
APPLICANT: Sutie, Janet L.
TILE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE DNUMBER OF SEQUENCES:
ADDRESSEE: No. 6075185art*
CTTW.
CTTW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIPO
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBAP FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JWN-1995
APPLICATION NUMBER: US 07/772,027
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
ARRESTRENCE/DOCKET NUMBER: 38,241
REGISTRATION NUMBER: 38,241
RESTRENCE/DOCKET NUMBER: 38,241
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRONE: (919) 541-8689
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUDRESSEE: NO. 6075185artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
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Patent No. 6121014
GENERAL INPORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 346 amino acide TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 SGPPSGARRRNCYE 15
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; MOLECULE TYPE: protein
US-08-459-504B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-08-459-444-19
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GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Gueller, Karl J.
APPLICANT: Gueller, Karl J.
APPLICANT: Gorley, Nell C.
TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEB: INCYTE PHARMACEUTICALS, INC.
STREET: All ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                       SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
RPPLICATION DATA:
FILLING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
57;
                                                                                                                                                     APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
FILING DATE: 02-UNN-1995
APPLICATION NUMBER: US 07/951,715
APPLICATION NUMBER: US 07/772,027
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-No. 6720488-2001
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REPERENCE/DOCKET NUMBER: S-18805I
TELEPHONE: (919)541-8689
TELEPK: (919)541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
  OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-09-083-521-2
Sequence 2, Application US/09083521
; Patent No. 6048970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: Herewith CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTATION UNDHERE: 39,132
REFERENCE/DOCKET NUMBER: PF-01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 49.4%;
Best Local Similarity 42.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Sequence 19, Application US/09988462

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

Besai, Nalini M.

Lewis, Kally S.

Kramer, Vance C.

Warren, Gregory W.

Evola, Stephen V.

Crossland, Lyle D.

Wright, Martha S.

Merlin, Ellis J.

Launis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                      COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,422
FILING DATE: 1.-Apr-2000
CLASSIFICATION NUMBER: US 08/459,595
FILING DATE: 0.2-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/712,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.4%; Score 43; DB 3; Length 346; 42.9%; Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805H
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 346 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                             ZIP: 27709
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 SGPPSGARRNCYE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 AAPPOAGRRRRCHO 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: NC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-988-462-19
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Sequence 22424 Application US/0925291A

Pacquence 22424 Application US/0925291A

Pacquence 22424 Application US/0925291A

Pacquence 22424 Application US/0925291A

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR PALLOR APPLICATION NUMBER: US/00/04,190

PRIOR FILING DATE: 1999-07-18

PRIOR FILING DATE: 1999-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22424

LENGTH: 613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.3%; Score 42; DB 4; Length 613; 58.3%; Pred. No. 1.4e+02; ive 1; Mismatches 4; Indels
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                                                                           COMPUTER: FIDDY GIRE
COMPUTER: FIDDY GIRE
COMPUTER: FIDDY GIRE
COMPUTER: FIDDY GIRE
SOCTAMEN: PRE-DICATION
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/029,679
FILING DATE: CONCURRENTLY HERWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,679
FILING DATE: 30-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,056
FILING DATE: 02-0CT-1996
FILING DATE: 10-SEP-1996
FILING DATE: 10-SEP-1996
APPLICATION NUMBER: US 60/025,719
FILING DATE: 10-SEP-1996
APPLICATION NUMBER: US 60/025,719
FILING DATE: 10-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, MATK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:272
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative (
                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 314 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 YSGPPPRARPGTC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YSGPPSGARRRNC 13
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597 SATPGGPRRKNC 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-927-219-6
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                   ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Pseudo
US-09-252-991A-22424
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US-09-252-991A-18128
i Sequence 18128, Application US/09252991A
patent No. 6551795;
Patent No. 6551795;
GENERAL INFORMATION:
I APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
I TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
I TITLE OF INVENTION: US/09/252,991A
FULL REFERENCE: 107196.136
CURRENT FILING DATE: 1998-02-18
PRIOR PRILING DATE: 1998-02-18
PRIOR PLILING DATE: 1998-02-18
PRIOR PLILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SENGIB: NO 18128
LENGTH: 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bell, Graeme I.
APPLICANT: Bell, Graeme I.
APPLICANT: Bell, Graeme I.
APPLICANT: Managate, Kazuya
APPLICANT: Kaisaki, Pamela J.
APPLICANT: Kaisaki, Pamela J.
APPLICANT: Kaisaki, Pamela J.
APPLICANT: Kaisaki, Pamela J.
APPLICANT: Monzel, Stephen
TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA
TITLE OF INVENTION: AND HNF-4ALPHA
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
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STREET: P.O. Box 4433
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Patent No. 6187533
information for SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 410 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: BRSTTUT03 CLONE: 1999442
                                                                                                                                                                                                                                                                                                                Conservative
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182 SGPGTPARRRC 193
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Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserval
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US-08-927-219-6
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Search completed: March 3, 2005, 14:00:55 Job time: 42 secs

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                                                                                                                                                                                                                          March 3, 2005, 13:57:17 ; Search time 134 Seconds (without alignments) 36.833 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/PCT_RPW PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_RPW PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/PCT_RPW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBGOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO6_PUBGOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
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                                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1391452 segs, 329044822 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                      OM protein - protein search, using sw model
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87
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YSGPPSGARRRNCYE 15
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
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Description	Sequence 401, App	Sequence 245359,	Sequence 126355,	Sequence 371, App	Sequence 968, App	Sequence 172815,	Sequence 170072,	Sequence 60305, A	Sequence 62618, A	Sequence 64572, A	Sequence 48971, A		Sequence 40066, A
ΩΙ	US-10-157-031-401	US-10-424-599-245359	US-10-437-963-126355	US-10-363-616-371	US-09-925-300-968	US-10-437-963-172815	US-10-424-599-170072	US-10-425-114-60305	US-10-282-122A-62618	US-10-282-122A-64572	US-10-425-114-48971	US-10-424-599-203545	US-10-425-114-40066
	14	15	16	15	6	16	15	15	15	15	15	15	15
% Query Match Length DB ID	320	278	1278	271	291	316	259	336	1167	1184	97	103	289
& Query Match	100.0	56.3	55.2	54.0	54.0	54.0	52.9	51.7	51.7	51.7	50.6	50.6	50.6
Score	87	49	48	47	47	47	46	45	45	45	44	44	44
Result No.	-	7	m	4	2	9	7	80	6	10	11	12	13

US-10-424-599-245359
; Sequence 245359, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

14 43.5 S.O. 7 11 UG-10-22-599-215548 Sequence 215544, 14 43 43 44 41 12 15 15 UG-10-22-599-17799 Sequence 215544, 14 43 44 44 44 45 UG-10-22-599-17799 Sequence 215544, 14 43 49.4 125 16 UG-10-22-599-17799 Sequence 215544, 14 43 49.4 125 16 UG-10-22-599-17799 Sequence 215744, 14 43 49.4 125 16 UG-10-22-213-2 Sequence 215.4 Appl. 14 43 49.4 413 18 UG-10-22-213-2 Sequence 215.4 Appl. 22 43 49.4 413 19 UG-10-22-213-2 Sequence 215.4 Appl. 22 43 49.4 413 19 UG-10-22-213-2 Sequence 215.4 Appl. 22 43 49.4 413 19 UG-10-22-213-2 Sequence 215.4 Appl. 22 43 49.4 413 19 UG-10-22-213-2 Sequence 215.4 Appl. 22 43 49.4 413 19 UG-10-22-214-37C2 Sequence 215.4 Appl. 22 42 48.3 49.4 413 19 UG-10-22-114-4449 Sequence 195765, According to 10 UG-10-22-114-37C2 Sequence 195765, According to 10 UG-10-22-114-4444 Sequence 195775, Acco

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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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| Patent No. US20020151681A1
| GENERAL INFORMATION:
| APPLICANT: Craig Rosen,
| TILE OF INVENTION: Nucleic Acids, Proteins and Antibodies
| FILE REFERENCE: PA10.
| CURRENT APPLICATION NUMBER: US/09/925,300
| CURRENT APPLICATION NUMBER: US/09/925,300
| PRIOR FILING DATE: 2001-08-10
| PRIOR FILING DATE: 1999-03-12
| NUMBER OF SEQ ID NOS: 1890
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 271;
                                                                                                                                            ; Sequence 371, Application US/10363616;
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES;
; TILE BREERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT APPLICATION NUMBER: 09/654,935
; PRIOR APPLICANION NUMBER: 09/654,935
; RICH FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 9; Length 291;
Pred. No. 35;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 8; Conserv
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US-10-437-963-172815
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us-10-018-964-5

APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NOS: 285684
SEG ID NOS: 285684
TYPE: TT
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 126355
LENGTH: 1278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.3%; Score 49; DB 15; Length 278, 66.7%; Pred. No. 16;
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US-10-424-599-245359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT4530_2890C.1.pep
US-10-437-963-126355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)..(278)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1)..(1278)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 126355, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Baukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 PPSGVRKIECYE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 PPSGARRRNCYE 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-437-963-126355
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US-10-363-616-371
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CUKKEMY FILLING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-16
PRIOR PRIOR OFFICE APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2001-02-16
PRIOR DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR DATE: 2001-02-16
PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 2.7e+02;
1; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                                   Length 336;
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: LIB3606-028-E11_FLI.pep
US-10-425-114-60305
                                                                                                                                                                                                                                                                            Score 45; DB 15;
Pred. No. 82;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Mycobacterium bovis
US-10-282-122A-62618
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 SGPPSGARRNCYE 15
         NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 60305
LENGTH: 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 |: |:||||||
88 PADAKRRNCY 97
                                                                                                                                                                                                                                                                                                                                                                                                  5 PSGARRRNCY 14
                                                                                               TYPE: PRT
ORGANISM: Zea mays
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Can Yongwei
TITLE OF INVENTION: SOy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 170072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 316;
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Pred. No. 45;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT3847_124590C.1.pep
US-10-424-599-170072
                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT4530_70914C.1.pep
US-10-437-963-172815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 47; DB 16;
Pred. No. 38;
1; Mismatches 4
                                                                                                                                                                                                                                                                                   LOCATION: (1)...(316)
OTHER INFORMATION: unsure at all Xaa locations FEATURE:
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
LENGTH: 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 60305, Application US/10425114
Ubblication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YSGPPSGARRRNC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 52.9
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 PPSSSGKRNCY 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 PPSGARRRNCY 14
                                                                                                                                                                                                               ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Glycine max
                                                                                                                                                                                                                                                                         NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-424-599-170072
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                                                                                                                                                                                                                                                 FEATURE:
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Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
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Best Local Similarity 58.30
Ti Conservative
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27 PPSGVHKIECYE 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-424-599-203545
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                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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| CURRENT APPLICATION NUMBER: US/10/282,122A |
| CURRENT FILING DATE: 2003-02-20 |
| PRIOR APPLICATION NUMBER: 60/200,948 |
| PRIOR PILING DATE: 2000-05-23 |
| PRIOR PELICATION NUMBER: 60/207,727 |
| PRIOR APPLICATION NUMBER: 60/207,727 |
| PRIOR PELICATION NUMBER: 60/207,727 |
| PRIOR PELICATION NUMBER: 60/230,335 |
| PRIOR PELICATION NUMBER: 60/230,347 |
| PRIOR PELICATION NUMBER: 60/230,347 |
| PRIOR APPLICATION NUMBER: 60/245,578 |
| PRIOR APPLICATION NUMBER: 60/253,625 |
| PRIOR APPLICATION NUMBER: 60/253,625 |
| PRIOR APPLICATION NUMBER: 60/253,625 |
| PRIOR PELING DATE: 2000-10-22 |
| PRIOR PELING DATE: 2000-11-27 |
| PRIOR PELING DATE: 2001-02-22 |
| PRIOR APPLICATION NUMBER: 60/269,308 |
| PRIOR PILING DATE: 2001-02-16 |
| PRIOR APPLICATION NUMBER: 60/269,308 |
| PRIOR APPLICATION NUMBER: 60/269,308 |
| PRIOR PILING DATE: 2001-02-16 |
| PRIOR APPLICATION NUMBER: 60/269,308 |
| PRIOR PILING DATE: 2001-02-16 |
| PRIOR APPLICATION NUMBER: 60/269,308 |
| PRIOR PILING DATE: 2001-02-16 |
| PRIOR APPLICATION NUMBER: 60/269,308 |
| PRIOR PILING DATE: 2001-02-16 |
| PRIOR PILING DATE: 2001-02-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Forsyth, R. APPLICANT: Xu, H. TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                           Sequence 64572, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Alone, Cheryl
APPLICANT: Alone, Nail
APPLICANT: Olleen, Kai
APPLICANT: Olleen, Kai
APPLICANT: Tawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
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Sequence 48971, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
334 AGPPDGYRERAAYE 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      335 AGPPDGYRERAAYE 348
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Matches 8; Conservative
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Sequence 203545, Application US/10424599
Sequence 203545, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE OF LAPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 203545
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 48971
LENGTH: 97
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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Value Selven E
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US-10-424-599-203545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 15;
Pred. No. 35;
1; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 15;
Pred. No. 37;
1; Mismatches 4;
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US-10-425-114-48971
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US-10-424-599-235980

US-10-424-599-235980

Sequence 235980, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

PILE REFERENCE: 38-21(53223) B

CURRENT FILING DATE: 2003-04-28

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 235980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ## Sequence 215744, Application US/10424599

## Sequence 215744, Application US/10424599

## Sequence 215744, Application US/10424599

## Publication No. US20040031072A1

## Repair CANT: La Rosa Thomas J

## APPLICANT: La Rosa Thomas J

## APPLICANT: Aco Yongwei

## TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

## TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

## PILE REPERBNCE: 38-21(5322)B

## CURRENT APPLICATION NUMBER: US/10/424,599

## CURRENT FILING DATE: 2003-04-28

## NUMBER OF SEQ ID NOS: 285684

## SEQ ID NO 215744
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                                                                                                                                                                     Score 44; DB 15; Length 289;
Pred. No. 1e+02;
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US-10-424-599-235980
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_36846C.1.pep
US-10-424-599-215744
                                       TYPE: PRT
ORGANISM: Glycine max
PEATURE:
OTHER INFORMATION: Clone ID: 700981026_FLI.pep
US-10-425-114-40066
                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%;
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Best Local Similarity 58.3%;
Matches 7; Conservative
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Best Local Similarity 66.7
Matches 10; Conservative
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ORGANISM: Glycine max
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49.4%; Score 43; DB 15; Length 46;

Query Match

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Best Local Similarity 54.5%; Pred. No. 25;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps

Oy 4 PPSGARRNCY 14

Db 34 PTSGSRKKSCY 44

Search completed: March 3, 2005, 14:12:01

Job time: 135 secs
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,32, 5, Appl 83, App 184, App 124483,

285, App 53450, A 112349, 252, App 5252, Ap

376, App 96, Appl

75153, A

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Total number

Searched:

Title: Perfect score: Sequence:

protein

Run on: Σõ

Scoring table:

65811, A

5073, Ap 12, Appl 4, Appli 1, Appli 129806,

15225, A 102582,

Appli

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Publication No. US20030108990A1
Publication No. US20030108990A1
Publication No. US20030108990A1
GENERAL INFORMATION:
APPLICANT: Baranova, A. V.
APPLICANT: Kozlov, A. P.
APPLICANT: Krokovskay, L. L.
TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences FILE OF INVENTION: In silico screening for phenotype-associated capacity CURRENT FILING DATE: 2002-05-30
CURRENT FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 415
SOFTWARE: Patentin version 3.1
SEQ ID NO 400
LENGTH: 2480
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Sequence 1931, Ap
Sequence 4156, Ap
Sequence 102517,
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Sequence 46584, A
Sequence 46585, A
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Sequence 55618, A
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Sequence 35317, A
Sequence 73, Appl
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Sequence 2235, Ap
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                                                                       8 US-10-157-031-400
8 US-10-723-860-7932
8 US-10-473-126-183
8 US-10-473-126-184
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8 US-10-473-126-184
8 US-10-473-126-184
8 US-10-473-126-184
8 US-10-425-115-124483
9 US-10-287-136-128-13812
9 US-10-128-714-2552
5 US-10-128-714-2552
5 US-10-128-714-2552
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9 US-10-425-115-41288
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-157-031-400
                                                                                                                                                     Result
                                                                                                                                                                                                                                                      Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-MODEL=frame+ p2n.model -DEV=xlp
-Q=/Cgn2 1/USFTO spool p/US10018964/runat_03032005_114709_21446/app_query.fasta_1.199
-DB=Published Applications NA -QFWT=fastap -SUFFTX=rnpb -MIRWATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITE=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUFFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10018964 @CGN 1 1 723 @runat 03032005_114709_21446
-NCPUG= ICPU=3 -NO MWAP -LARGEQUERY NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGARDOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                        March 7, 2005, 09:09:13 ; Search time 492 Seconds (without alignments) 180.910 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications NA:*

1: /cgn2_6/ptodata/1/Pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/Pubpna/PET_NEW_PUBL.seq:*
3: /cgn2_6/ptodata/1/Pubpna/DET_NEW_PUBL.seq:*
4: /cgn2_6/ptodata/1/Pubpna/US06_PUBCOMB.seq:*
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9: /cgn2_6/ptodata/1/Pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/Pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/Pubpna/US09_PUBCOMB.seq:*
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19: /cgn2_6/ptodata/1/Pubpna/US10F_PUBCOMB.seq:*
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19: /cgn2_6/ptodata/1/Pubpna/US10F_PUBCOMB.seq:*
21: /cgn2_6/ptodata/1/Pubpna/US10F_PUBCOMB.seq:*
22: /cgn2_6/ptodata/1/Pubpna/US10F_PUBCOMB.seq:*
22: /cgn2_6/ptodata/1/Pubpna/US10F_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                            nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Listing first 45 summaries
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87
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Database

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Sequence 184, Application US/10473126

Publication No. US20040234973A1

Publication No. US20040234973A1

APPLICANT: Epigenomics AG

TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
TITLE OF INVENTION: proliferative disorders

FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126

CURRENT FILING DATE: 2003-09-26

NUMBER OF SEQ ID NOS: 1258

EBOT ID NO 184

LENGTH: 3025
                                                                                                                                                                                                                                                                                                                                                                                                                                                    hematopoietic cell
                                                                                                                                                                                                                                                                                                                                                         Sequence 183, Application US/10473126
Publication No. US20040234973A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 183
LENGTH: 3025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-473-126-183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                j OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-184
                                                                                                                                                                                                                                                                     1 TyrSerGlyProProSerGlyAlaArgArgArgAsnCysTyrGlu 15
                                                                                                                                                                                                                                           1 TyrSerGlyProProSerGlyAlaArgArgArgAsnCysTyrGlu 15
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Conservative:
Mismatches:
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Matches:
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                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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US-10-473-126-184/c
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US-10-473-126-183
                                          Alignment Scores:
Pred. No.:
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Pred. No.:
    US-10-473-126-45
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US-10-473-126-45
Sequence 45, Application US/10473126
Sequence 45, Application US/10473126
Sequence 45, Application US/10473126
Sequence 75, Publication No. US20040234973A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
TITLE OF INVENTION: proliferative disorders
TITLE OF INVENTION: UNMBER: US/10/473,126
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
MUMBER OF SEQ ID NOS: 1258
                                                                                                                                                                                                                                                                                                                                                       Sequence 7932, Application US/10723860
| Publication No. US2004025366A1
| GENERAL INCORMATION:
| APPLICANT: Aziz, Natasha
| TILLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma, Compositions &
| TILLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
| TILLE OF INVENTION: NUMBER: US/10/723,860
| CURRENT FILING DATE: 2003-11-26
| PRIOR APPLICATION NUMBER: 60/429,739
| PRIOR FILING DATE: 2002-11-26
| WUMBER OF SEQ ID NOS: 8393
| SOFTWARE: Patentin Version 3.2
| SEQ ID NO 7932
                                                                                                                                                                                                                                                                   850 TACAGGGGCCCCCGAGCGGGGGCGCCCGGCGGAACTGCTACGAA 894
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                                                                             Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
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i LOCATTON: (2534)..(2743)
i OTHER INPORMATION: n is a, c, g,
US-10-723-860-7932
                                                      0.000198
87.00
100.00%
100.00%
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87.00
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ORGANISM: Homo sapiens
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ORGANISM: Homo Sapiens
                                                                                              Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
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JS-10-157-031-400
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Pred. No.:
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LENGTH: 3025
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DB:
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Best Local Similarity:
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Sequence 12546, Application US/10357930

Publication No. US20040259086A1

GENERAL INFORMATION:
APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: DEBNIFFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: LIDENTIFFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MILOOPECN
CURRENT FILING DATE: 2003-02-04
PRIOR PPLICATION NUMBER: 09/183,319
PRIOR PILING DATE: 2000-02-17
PRIOR PLLING DATE: 2000-02-17
PRIOR PLLING DATE: 2000-03-16
PRIOR PPLICATION NUMBER: 60/183,319
PRIOR PLLING DATE: 2000-03-16
PRIOR PPLICATION NUMBER: 60/207,454
PRIOR PPLICATION NUMBER: 60/207,454
PRIOR PLLING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR PLLING DATE: 2000-06-09
                                                                                                                                                                                                                                                                                          Sequence 124483, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: LR Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Tou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/2020 B
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 124483
LENGTH: 461
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Matches:
Conservative:
Mismatches:
Indels:
       Conservative:
                          Mismatches:
Indels:
Gaps:
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US-10-425-115-124483
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64.37%
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Best Local Similarity:
Query Match:
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ORGANISM: Zea mays
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Percent Similarity:
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APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
ITLE OP INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
ITLE OP INVENTION: Methods of Use
FILE REFERENCE: 10182-018-99
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
FRIOR APPLICATION NUMBER: US 60/285,697
FRIOR APPLICATION NUMBER: US 60/285,697
FRIOR PILING DATE: 2001-04-27
FRIOR PLING DATE: 2001-04-27
FRIOR PLING DATE: 2001-04-27
FRIOR PLING DATE: 2001-06-05
FRIOR PLING DATE: 2001-05-06
FRIOR FILING DATE: 2001-07-09
FRIOR FILING DATE: 2001-08-31
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CRGANISM: Aspergillus fumigatus
US-10-128-714-7252
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Best Local Similarity:
Query Match:
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Pred. No.:
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Squence 2552, Application US/10128714

Squence 2552, Application US/10128714

GENERAL INFORMATION:

APPLICANT: Jiang, Bo
APPLICANT: Jiang, Bo
APPLICANT: Tishkoff, Daniel

APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lemieux, Sebsstien M
APPLICANT: Lemieux, Sebsstien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
TITLE OF INVENTION: Wethods of Use
TITLE OF INVENTION WHERE: US 60128, 114

CURRENT APPLICATION NUMBER: US 60/285, 697

PRIOR FILING DATE: 2001-04-27

PRIOR PRILING DATE: 2001-04-27

PRIOR PILING DATE: 2001-04-27

PRIOR PILING DATE: 2001-04-27

PRIOR PILING DATE: 2001-04-27

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-08-31

NUMBER OF SEQ ID NOS: 8603

SEQ ID NOS: 8603

SEQ ID NOS: 8603

LENGTH Sec
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Matches:
Conservative:
Mismatches:
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Gaps:
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Matches:
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8-10-128-714-7252
Sequence 7252, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
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; ORGANISM: Aspergillus fumigatus
US-10-128-714-2252
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52.00
91.67%
75.00%
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APPLICANT: Hu, Wenqi
APPLICANT: Tahkoff, Daniel
APPLICANT: Zamudio, Carlos
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Best Local Similarity:
Query Match:
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Best Local Similarity:
US-10-282-122A-13812
                                               Alignment Scores:
Pred. No.:
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APPLICANT: Li, Ping
TITLE OF INVENTION: Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 48056
LENGTH: 2328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengi
APPLICANT: Hu, Wengi
APPLICANT: TishkofL Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
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Matches:
Conservative:
Mismatches:
Indels:
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US-10-437-963-48056
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Conservative:
Mismatches:
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PRIOR FILING DATE: 2001-04-23
PRIOR FILING DATE: 2001-04-27
PRIOR PILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR PILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR PILING DATE: 2001-06-09
PRIOR PILING DATE: 2001-09-09
PRIOR PILING DATE: 2001-09-09
PRIOR PILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SEQ ID NO 252
LENGTH: 2908
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51.00
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51.00
90.00$
90.00$
58.62$
                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Eamadio, Carlos
APPLICANT: Eamadio, Carlos
APPLICANT: Lemieux, Sebastien M
ITILE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
ITILE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-99
CURRENT PILING DATE: 2002-04-23
PRIOR PPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR PLING DATE: 2001-04-27
PRIOR PLING DATE: 2001-04-27
PRIOR PLING DATE: 2001-06-05
PRIOR PLING DATE: 2001-06-05
PRIOR PLING DATE: 2001-07-09
PRIOR PLING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
NUMBER OF SEQ ID NOS: 8603
NUMBER OF SEQ ID NOS: 8603
PRIOR PLING DATE: Patentin version 3.1
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Matches:
Conservative:
Mismatches:
Indels:
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wei
APPLICANT: Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                          Sequence 6252, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Aspergillus fumigatus
                    66.6
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  Alignment Scores:
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LENGTH: 908
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Sequence 5252, Application US/10128714

Sequence 5252, Application US/10128714

GENERAL INFORMATION:

APPLICANT: Jiang, Bo
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Excelkin, Alexey M
APPLICANT: Excelkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Usely 500 of Use
TITLE OF INVENTION NUMBER: US 60/285,697
PRIOR PAPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/285,890
PRIOR APPLICATION NUMBER: US 60/285,890
PRIOR APPLICATION NUMBER: US 60/285,890
PRIOR PRILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR PRILING DATE: 2001-08-31
SOCTHARE: PARENTLY PAPEL SOUTH OF SECTION OF SECTIO
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Gaps:
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; ORGANISM: Aspergillus fumigatus
US-10-128-714-5252
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US-10-128-714-5252
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1497 CCACCGAGTGGGTGGAGAGGAGGAACTGC 1526

Search completed: March 7, 2005, 11:37:51 Job time : 494 secs

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 580)
E 1 (bases 1 to 580)
E 1 (bases 1 to 580)
E NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM200 row: p column: 18
High quality sequence stop: 579.
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CH261-92J
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CC456912
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AUTHORS
TITLE
JOURNAL
COMMENT
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Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-0=/Cqn2 1/USPTO spon.model -DEV=xlp
-0=/Cqn2 1/USPTO spon.dlp/USR 1018964/runat 03032005 114707 21373/app_query.fasta_1.199
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-USRF-WISD -NORM=ext -NEGS SCORES=0 -WAIT -SPSPLOXE=100 -LONGLOG
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -SPSPLOXE=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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(without alignments)
183.945 Million cell updates/sec
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BG829220
                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                              nucleic search, using frame_plus_p2n model
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Listing first 45 summaries
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Conservative: Mismatches: Indels:

Gaps:

Matches:

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/clone lib="NIH MGC_17"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
/note="Organ: muscle; Vector: poTB7; Vector: poTB7;
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Email: cgapbs-r@mail.nih.gov
Tisaue Procurement: ATC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLCM1807 row: 1 column: 01
High quality sequence stop: 677.
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/organism="Homo sapiens"
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BG829220
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// (db xref="taxon:9606"
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/clone="IMAGE:53:812"
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Site_2: Khoi; cDNA made by O algo-dr priming.
Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp in a reason insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis Kit (Stratagene) and Superscript II RT (Life Technologies)."
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601176586P1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531812 5',
mRNA_sequence.
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MH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: Ggapbs-remail.nih.gov
Tissue Procurement: ArCe
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
High quality sequence stop: 607.
Location/Qualifiers
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'lab_host="DH10B (phage-resistant)"
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678 115 0 0 0

Length: Matches: Conservative: Mismatches: Indels:

Alignment Scores: Pred. No.:

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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 9100 GENYX cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
                                     2 (bases 1 to 963)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Murphy,B.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
Location/Qualifiers
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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/tissue_type="Placenta Cot 25-normalized"
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        Science 302 (5652), 1960-1963 (2003)
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                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DN /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                         /gene="MYOD1"
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CR612159.1 GI:50492966
HTC; CNSLT_CDNA.
HOMC sapiens (human)
Homc sapiens
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      Pan troglodytes MYOD1 gene, VIRTUAL TRANSCRIPT, partial sequence,
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Pan troglodytes
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1 (bases 1 to 958)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todh, M.A., Tanenbaum, D.M., Civello, B., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
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<l...>958
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genomic survey sequence.
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AY399565.1 GI:39755554
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Alignment Scores:

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

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DEFINITION

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// (db xref="taxon:9606"
/clone="IMAGE:411538"
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.
E 1 (bases 1 to 520)
INH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Arcc
CONA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM999 row: h column: 03
High quality sequence stop: 520.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                            283 TACAGCGCCCCCCAGTGGTGCCCGGCGGAACTGCTACGAC 327
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/organism="Homo sapiens"
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Other_GSSS: CH240.107G14.TV

Contact: Harris Lewin

Other_GSSS: CH240.107G14.TV

Contact: Harris Lewin

Liou W. Gregory Dr., Urbana Champaign

1201 W. Gregory Dr., Urbana, IL 61801, USA

Fax: 217 244 5617

Email: h-lewin@uiuc.edu

Clones are derived from the bovine BAC library CHORI-240

(http://www.chori.org/bacpac/bovine240.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

(http://www.chori.org/bacpac/ordering_liformation.htm). This work

was undertaken as part of the International Bavine BAC Mapping

Consortium (IBBMC) by by University of Illinois at Urbana

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In (Dassel I to 529)

Larkin, D.M., Everts-van der Wind, A., Rebeiz, M., Schweitzer, P.,

Bachman, S., Green, S., Campos, E.J., Benson, L.D., Edwards, J., Liu, L.,

Womack, J.E., de Jong, P.J. and Lewin, H.A.

A Cattle-Human Comparative Map Built with Cattle BAC-ends and Human
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CH240 107614.TJ CHORI-240 Bos taurus genomic clone CH240_107614,
genomic survey sequence.
BZ940212
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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/organism="Bos taurus"
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/lab host="DH108 [phage-resistant)"
/clone_lib="NIH_MGC_17"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
/note="Organ: muscle; Vector: potigo-dT priming.

Directionally cloned into EcoRI/Xhol sites using the following 5' adaptor: GGGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                     BE298779 11near EST 20-JUL-2000 601119328F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029047 5',
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                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
I (bases I to 614)
NHF. WGC http://mgc.ndi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 805)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Preparation: Ling Hong/Rubin Laboratory DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM8 row: h column: 08
High quality sequence stop: 611.
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Mismatches:
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                                                                                                                 BE298779.1 GI:9182524
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/nol_type="mRNA"

/db_txef="txexon:9606"

/dlone='IMAGE:2960106"

/tissue_type="rhabdomyosarcoma"

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/tab_host="DH108 (phage-resistant)"

/dlone_lib="WHH MGC_17"

/note="Organ: muscle; Vector: pOTB7; Site_l: EcoRI;

/note="Organ: muscle; Vector: poTB7; Vector: poTB7; Site_l: EcoRI;

/note="Organ: muscle; Vector: poTB7; 
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 807)
                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov
Plate: LLCM52 row: o column: 19
High quality Sequence stop: 748.
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Email: Gapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM999 prow: p column: 24
High quality sequence stop: 698.
National Institutes of Health, Mammalian Gene Collection (MGC)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Conservative:
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Homo sapiens (human)
Homo sapiens
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                               /clone="IMAGE:4111751"
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/clone lib="WIH MGC 17"
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Site_2: Xhoi; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the birectionally cloned into EcoRI(XhoI sites using the following 5' adaptor: GGGAGG(G). Size selected >SOObp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University
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Contact: Robert Strausberg, Ph.D.
Email: capabe=romail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Presyed by: The I.M.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.G.E. Consortium/LLNL at:
Pittp://image.llnl.gov
Plate: LLCM1842 row: i column: 12
High quality sequence stop: 769.
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1 (bases 1 to 813)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mismatches:
Indels:
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Matches:
Ltype="mRNA"
xref="taxon:9606"
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BI115390
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1055)

2 Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization

LD May 5, 2003 this sequence version replaced gi:30372341.

On May 5, 2003 this sequence version replaced gi:30372341.

Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremeieux, CP 5706 - 91057 ENRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCWVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 08-APR-2004
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BX359424 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI057XKI0 5-PRIME, mRNA sequence.
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digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Matches:
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This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. L. (basea 1 to 406).
Marra, M., Hilier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., The Mashu-NcI Mouse EST Project 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seg primer: Primer name ambiguous
High quality sequence stop: 358.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          correct orientation)
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Query Match:
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AUTHORS
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                                                                                                            BI114827 1000 bp mRNA linear EST 26-JUN-2001
602861387F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:5020629 5',
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NIH-WGC http://mgc.nci.nih.gov/.
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ve32c09.y1 Ko mouse embryo 11 5dpc Mus musculus cDNA clone
IMAGE:819856 5' similar to gb:M18779 Mouse myoblast D1 (MOUSE);,
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CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1837 row: n column: 22
High quality sequence stop: 741.
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: ATCC
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Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                            BI114827.1 GI:14565728
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                                                                                                                                                                                                                                                                                Homo sapiens (human)
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AI428972
AI428972.1 GI:
                                                                                                                                                                      mRNA sequence.
BI114827
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Best Local Similarity:
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                     LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                         ORGANISM
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DEFINITION
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                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
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AUTHORS
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AI428972
                                                            RESULT 14
                                                                                     BI114827
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1 TyrSerGlyProProSerGlyAlaArgArgArgArgAsnCysTyrGlu 15
                                                                                                                                               35 TACAGCGCCCCCCAAGCGGCCCCCGGCGGCAGAATGGCTACGAC 79
406
111
2
0
0
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                 US-10-018-964-3_COPY_1_15 (1-15) x AI428972 (1-406)
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